

11729.1 contg

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTTGTGTTTGTGTTTGTGTTT
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CCGCCTCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCCGCCAC
CAGCTCAGCTAATTTTTTTTGTATTTTGTAGTAGAGACAGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAA
CTCCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACG
CCCGGCCCCCAAAGCTGTTTCTTTTGTCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGAC
GTGACTGCCAGCAAGCTCAGTCACTCCGTGGTC

11729-45.21.21.cons1

TAGGATGTGTTGGACCCTCTGTGTCAAAAAAACCTCACAAAGAATCCCCTGCTCATTACAGAAGAAGATGC
ATTTAAATATGGGTATTTTCACTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTGAGAAGAGATTG
AATACCTGCTTAAGAAGCTTACAGAAGCTATGGGAGGAGGTTGGCAGCAAGAACAATTTGAACATTATAAAA
TCACTTTGATGACAGTAAAAATGGCCTTTCTGCATGGGAATTATTGAGCTTATTGGAAATGGACAGTTTA
GCAAAGGCATGGACCGGCAGACTGTGTCTATGGCAATTAATGAAGTCTTTAATGAACTTATATTAGATGTGT
TAAAGCAGGGTTACATGATGAAAAAGGGCCACAGACGGAAAACTGGACTGAAAGATGGTTTGTACTAAAA
CCCAACATAATTTCTTACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTTGGATGAAAAT
TGCTGTGTAGAGTCCTTGCCTGACAAAGATGGAAA

11729-45.21.21.cons2

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTTGTGTTTGTGTTTGTGTTT
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CCGCCTCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCCGCCAC
CAGCTCAGCTAATTTTTTTTGTATTTTGTAGTAGAGACAGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAA
CTCCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACG
CCCGGCCCCCAAAGCTGTTTCTTTTGTCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGAC
GTGACTGCCAGCAAGCTCAGTCACTCCGTGGTC

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TCTTTTCTTTTCGATTTTCTTCAATTTGTCACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTAT
TATAGCTTTCTCTGAGTTCCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTT
TCAAGAGCATCTAATTGTTCTTTAAGTCTTTGGCATAATTCTTCTTTTCTGATGACTTTTATGAAGTAACT
GATCCCTGAATCAGGTGTGTTACTGAGCTGCATGTTTTAATTCTTTCTGTTTAAATAGCTGCTTCTCAGGGACC
AGATAGATAAGCTTATTTTGATATTCCTTAAGCTCTTGTTGAAGTTGTTTGATTTCCATAATTTCCAGGTCACA
CTGTTTATCCAAACTTCTAGCTCAGTCTTTTGTGTTTGCTTCTGATTTGGACATCTTGTAGTCTGCCTGAG
ATCTGCTGATGXTTCCATTCACTGCTTCCAGTTCAGGTGGAGACTTXXCTTCTGGAGCTCAGCCTGACA
ATGCCTTCTTGXTCCCT

Fig. 1A

11731.2contig

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCCACAGCGATGAATGG
AGGGCCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACC
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AGCTGAAATATGGGCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTA
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CTATGTTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCCAATCTGTCCATTCATCAGCCAT
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TGCTGCTCCCCTAGTGCCTTCTGTTAGTA

11734.1contig

AATAGATTTAATGCAGAGTGTCAACTTCAATTGATTGATAGTGGCTGCCTAGAGTGCTGTGTTGAGTAGGTT
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GAAACCACAGGACCAAGAGCTGCCACTGGTGCTGGCACCAGCTCCACCAAGGCCAGCGAAGAGCCCAAAT
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CTGCAGCCTTCAAATCCGCTTCCATCGCCTCTCGGTAC

11734.2contig

GCCAAGAAAGCCCGAAAGGTGAAGCATCTGGATGGGGAAGAGGATGGCAGCAGTGATCAGAGTCAGGCTT
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GTCCCATAGCCTTTTGGGCCCCGAGGGCATCAAGGACTCGGTTGGCTGCTTGGGCCCCGAGAGCCTTGCT
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TTTTGGCTAAAGACCAGACGAAGATTCCCATCAAGCGCTCGGACATGCTGAAGGACATCATCAAAGAATAC
ACTGATGTGTACCCCGAAATCATTGAACGAGCAGGCTATTCTTGAGAGAAGGTATTTGGGATTCAATTGAAG
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11736.1contg

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TTCAAGAAGTGAAGGGTTTCCAGAGTATAGCTACACTATTGCTTGCCTGAGGGTGACTACAAAATTGCTTGC
TAAAGGTTAGGATGGGTAAAGAATTAGATTTTCTGAATGCAAAAATAAAATGTGAACTAATGAACTTTAGGT
AATACATATTCATAAAATAATTATTCACATATTTCTGATTTATCACAGAAATAATGTATGAAATGCTTTGAGTT
TCTTGGAGTAACTCCATTACTCATCCCAAGAAACCATATTATAAGTATCACTGATAATAAGAACAACAGGAC
CTTGTCATAAATTCTGGATAAGAGAAATAGTCTCTGGGTGTTTGXTCTTAATTGATAAAATTTACTTGTCCATC
TTTTAGTTCAGAATCACAAAA

"REPLACEMENT SHEETS"

11736.2contig

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CTCTGTGACCTGTTTGTACAGGTCCATGATGAGGTAAACAATACACTGAGTATAAGGGTTGTTTGTAAAC
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TCCTTTTTTTCATTTTCATGTTCTGAGTTACCTATTTTTATTGCATTTTACAAAAGCATCCTTCCATGAAGGACC
GGAAGTTAAAAACAAAGCAGGTCTTTATCACAGCACTGTCGTAGAACACAGTTCAGAGTTATCCACCCAAG
GAGCCAGGGAGCTGGGCTAAACCAAGAATTTTGCTTTTGGTTAATCATCAGGTACTTGAGTTGGAATTGTT
TTAATCCCATCATTACCAGGCTGGAXGTG

11739-1&2

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TGGACAACTACTTTTCCAGAACAGAAAGGAAACTCATGCATCAGAAAAGGTGACTAATAAAGGTACCAGAAG
AATATGGCTGCACAAATACCAGAATCTGATCAGATAAAACAGTTTAAGGAATTTCTGGGGACCTACAATAAA
CTTACAGAGACCTGCTTTTTGGACTGTGTTAGAGACTTCACAACAAGAGAAGTAAACCTGAAGAGACCACC
TGTTTCAAGAACATTGCTTACAGAAATATTTAAAAATGACACAAAGAATATCCATGAGATTTTCAAGGAATATCATA
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GCTATTTACCAGGAATAATCACAATAGAAGGTCTTATTGTTTCAAGTAAATAAAGATGCAACATTTGTTGAG
GCCTTATGATTCAGCAGCTTGGTCACTTGATTAGAAAAATAAACCATTGTTTCTTCAATTGTGACTGTTAATTT
TAAAGCAACTTATGTGTTTCGATCATGTATGAGATAGAAAAATTTTTATTACTCAAAGTAAATAAATGGA

11740.1.contig

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CCAATTTTATGAAAACGACAATTTAATCCAAGAATCACTTTTGTAAATGAAGCTAGCAAGTGATGATATGAT
AAAATAAACGTGGAGGAAATAAAAACACAAGACTTGGCATAAGATATATCCACTTTTGTATTAACCTTGTGA
AGCATATTCTTCGACAAATTGTGAAAGCGTTCCTGATCTTGCTTGTCTCCATTTCAAATAAGGAGGCATATC
ACATCCCAAGAGTAACAGAAAAAGAAAAAGACATTTTTGCATTTTGAAGATGAACCAAAGACACAAAACAAA
ACGAACAAAGTGTCATGTCTAATTCTAGCCTCTGAAATAAACCTTGAACATCTCCTACAAGGCACCGTGATT
TTTGTAATTCTAACCTGAAGAAATGTGATGACTTTTGTGGACATGAAAATCAGATGAGAAAACCTGTGGTCTTT
CCAAAGCCTGAACTCCCCTGAAAACCTTTGCA

11766.1.contig

CTGGGATCATTCTCTTGATGTCATAAAAGACTCTTCTTCTTCTCTTCATCCTCTTCTTCATCCTCTTCTGTA
CAGTGCTGCCGGGTACAACGGCTATCTTTGTCTTTATCCTGAGATGAAGATGATGCTTCTGTTTCTCCTACC
ATAACTGAAGAAATTTGCTGGAAGTCGTTTGACTGGCTGTTTCTCTGACTTCACCTTCTTTGTCAAACCTGA
GTCTTTTACCTCATGCCCCCTCAGCTTCCACAGCATCTTCATCTGGATGTTTATTTTCAAAGGGCTCACTGA
GGAACTTCTGATTCAGAGGTGGAAGAGTCACTGTGATTTTTCTCCTCATTTTGCTGCAAATTTGCCTCTTG
CTGTCTGTGCTCTCAGGCAACCCATTTGTTGTATGGGGGCTGACAAAGAAACCTTTGGTCGATTAAGTGG
CCTGGGTGTCCAGGCCCATTTATATTAGACCTCTCAGTATAGCTTGGTGAATTTCCAGGAAACATAACACC
ATTCATTCGATTAACTATTGGAATTGGTTTT

11766.2.contig

GAGGGTTGGTGGTAGCGGCTTGGGGAGGTGCTCGCTCTGTGGTCTTGCTCTCTCGCACGCTTCCCCCGG
CTCCCTTCGTTTCCCCCCCCCGGTGCGCTGCGTGCCGGAGTGTGTGCGAGGGAGGGGGAGGGCGTCCG
GGGGGTGGGGGGAGGCGTTCGGTCCCCAAGAGACCCGCGGAGGGAGGCGGAGGCTGTGAGGGACTCC
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TTAAAGGCTATTTTATTTTCAAACCTGGAGAAAGTGATGGATGATTTCAGAACTTCAGCTCCTGAGCCAAGAG
GTCCTCCCAACCCTAATGTCTGA

11773.2.contig

AAGCAGGCGGCTCCCGCGCTCGCAGGGCCGTGCCACCTGCCCCGCCGCGCTCGCTCGCTCGCCCCG
CGCGCCGCGCTGCCGACCGCCAGCATGCTGCCGAGAGTGGGCTGCCCCGCGCTGCCGXTGCCG

11775-1&2

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AACGTGAAGATTAACCTAATTGTCAAATATTCCTCATTGCCCAAATCAGTATTTTTTTTATTTCTATGCAAAA
GTATGCCTTCAAACCTGCTTAAATGATATATGATATGATACACAAACCAGTTTTCAAATAGTAAAGCCAGTCAT
CTTGCAATTGTAAGAAATAGGTAAAAGATTATAAGACACCTTACACACACACACACACACACACACGTGTGC
ACGCCAATGACAAAAACAATTTGGCCTCTCCTAAATAAGAACATGAAGACCCTTAATTGCTGCCAGGAGG
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AAAATGCCAATAATTTTTCGCTCCCACTTCTGCTGCTGCTGCTCTTCCACATCCTCACATAGACCCAGACCCGC
TGGCCCCTGGCTGGGCATCGCATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTACAGAAGCG
ATACACCAAATTGCCTGGTCCGTCATTGTCATAACCAGAGA

11777.1&2.cons

CAGACGGGGTTTCACTATGTTGGCTAGGCTGGTCTTGAACCTCCTGACTTCAGGTGATCTGCCTGCCTTGGC
CTCCCAAAGTGCTGGGATTACAGGCATAAGCCACTGCGCCCGGCTGATCTGATGGTTTCATAAGGCTTTTC
CCCCTTTTGTCTCAGCACTTCTCCTTCCTGCCGCCATGTGAAGAAGGACATGTTTGCTTCCCCTTCCACCACG
ATTGTAAGTTGTTTCTGAGGCCTCCCCGGCCATGCTGAACCTGTGAGTCAATTAAACCTCTTTCCTTTATAAA
TTATCCAGTTTTGGGTATGTCTTTATTAGTAGAATGAGAACAGACTAATACAACCCTTAAAGGAGACTGACG
GAGAGGATTCTTCCTGGATCCCAGCACTTCTCTGAATGCTACTGACATTCTTCTTGAGGACTTTAACTGG
GAGATAGAAAACAGATTCCATGGCTCAGCAGCCTGAGAGCAGGGAGGGAGCCAAGCTATAGATGACATGG
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CCTGTCCTTGAGAGCCAAGCCTCAATCACTGCTAGCCTCAAGTGTCCCCAAGCCACAGTGGCTAGGGGG
ACTCAGGGAACAGTTCCCAGTCTGCCCTACTTCTCTTACCTTTACCCCTCATACCTCCAAAGTAGACCATGT
TCATGAGGTCCAAAGG

11779.2.contig

AAGCGAGGAAGCCACTGCGGCTCCTGGCTGAAAAGCGGCGCCAGGCTCGGGAACAGAGGGAACGCGAAG
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GAAGCCCCGGGCTGAACGTGAGGCCGAGGCGCGGAGACGGGAGGAGCAGGAGGCTCGAGAGAAGGCGCA
GGCTGAGCAGGAGGAGCAGGAGCGACTGCAGAAGCAGAAAGAGGAAGCCGAAGCCCCGGTCCCGGGAAG
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AAAGGAGACCGCAGCTAACAATTCCGGCCCAGACCCTTGTGAAAGCTGTAGAGACTCGGCCCTCTGGGCT
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11781 & 37.cons

CTCTGTGGAAAACCTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCT
GATTACTGCAACACAGAGAACGAAGAAGAACTTTTCTCATACAGGATCAGCAGGGCCTCATCACACTGGG
CTGGATTCATACTACCCCAACACAGACCGCGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCA
GATGATGTTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCCAAGTTCCAGGAACTGGATTCTTTAACTAAC
TGACCATGGACTAGAGGAGATTTCTTCTGTGCGCCAGAAAGGATTTTCATCCACACAGCAAGGATCCACCTC
TGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTT
GAGTCCAACACCTTCCAAGAACAACAAAACCATATCAGTGTACTGTAGCCCCCTTAATTTAAGCTTTCTAGAAA
GCTTTGGAAGTTTTTGTAGATAGTAGAAAGGGGGGCATCACXTGAGAAAGAGCTGATTTTGTATTTAGGTT
TGAAAAGAAATAACTGAACATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAA
CTCAGAAATTAAGTTACTCAGAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCCATATA
CCCTTCCTTCTGGATTCACCAATTGTTAACATTTTTTCTCTCAGCTATCCTTCTAATTTCTCTAATTTCA
ATTTGTTTATATTTACCTCTGGGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTT
TGGATTTTCTGTGGTTTATGGCAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTG
ACCAGATTGTTTGGCTAACACATCCCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTTCAG
GATATTTTTCTCTACAATAAAGTAACAAT

11781-76-87-37

CTCTGTGGAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCT
GATTACTGCAACACAGAGAACGAAGAAGAACTTTTCCTCATACAGGATCAGCAGGGCCTCATCACACTGGG
CTGGATTCACTACACCCACACAGACCGCGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCA
GATGATGTTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCCAAGTTCCAGGAACTGGATTCTTTAACTAAC
TGACCATGGACTAGAGGAGATTTCTTCCTGTGCGCCAGAAAGGATTTTCATCCACACAGCAAGGATCCACCTC
TGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTT
GAGTCCAACACCTTCCAAGAACAACAAACCATATCAGTGTACTGTAGCCCCCTTAATTTAAGCTTTCTAGAAA
GCTTTGGAAGTTTTTGTAGATAGTAGAAAGGGGGGCATCACCTGAGAAAGAGCTGATTTTGTATTTAGGTT
TGAAAAGAAATAACTGAACATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAA
CTCAGAAATTAAGTTACTCAGAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCCATATA
CCCTTCCTTCTGGATTCACCAATTGTTAACATTTTTTCTCTCAGCTATCCTTCTAATTTCTCTAATTTCA
ATTTGTTTATATTTACCTCTGGGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTT
TGGATTTTCTGTGGTTTATGGCAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTG
ACCAGATTGTTTGGCTAACACATCCCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTGAG
GATATTTTCTCTACAATAAAGTAACAATTA

11784-1 & 2

GGACGACAAGGCCATGGCGATATCGGATCCGAATTCAAGCCTTTGGAATTAATAAACCTGGAACAGGGAA
GGTGAAAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGTGCACAGTTGAATGGGAAGTGTGGGTTT
AGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAACTGGTGGGAGGTCAAGTGGGGAAGTTGGT
GAATGTGGAATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAGCTTTCCTGACATGCAAGGATC
TACTTTAATTCACACTCTCATTAATAAATTGAATAAAAGGGAATGTTTTGGCACCTGATATAATCTGCCAGG
CTATGTGACAGTAGGAAGGAATGGTTTCCCCTAACAAAGCCCAATGCACTGGTCTGACTTTATAAATTATTTA
ATAAAATGAACTATTATC

11785.2.contig

GGCAGTGACATTCACCATCATGGGAACCACCTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCAC
CCAGTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTA
AGGTGCCAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAAAC
TTTCTAACTTCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAA
CTGGTGTTACCCAGAAAAACAGGAGCAATTAGAAATGTTTCCAATATTTCAAAGCTCCGCAACAGGATGTG
CTTTCCTTTGCCCATTTAGGGTTTCTTCTTTTCTTTCTTTTATTAACCACT

Fig. 1F

11718-1&2 cons

TGCGCTGAAAACAACGGCCTCCTTTACTGTAAAAATGCAGCCACAGGTGCTTAGCCGTGGGCATCTCAACC
ACCAGCCTCTGTGGGGGGCAGGTGGGCGTCCCTGTGGGCCTCTGGGCCACGTCCAGCCTCTGTCCTCT
GCCTTCCGTTCTTCGACAGTGTTCCCGGCATCCCTGGTCACTTGGTACTTGGCGTGGGCCTCCTGTGCTGC
TCCAGCAGCTCCTCCAGGXGGTCGGCCCGCTTCACCGCAGCCTCATGTTGTGTCCGGAGGCTGCTCACGG
CCTCCTCCTTCCTCGCGAGGGCTGTCTTCACCCTCCGGXGCACCTCCTCCAGCTCCAGCTGCTGGCGGGC
CTGCAGCGTGGCCAGCTCGGCCTTGGCCTGCCGCGTCTCCTCCTCARAGGCTGCCAGCCGGTCTCGAA
CTCCTGGCGGATCACCTGGGCCAGGTTGCTGCGCTCGCTAGAAAGCTGCTCGTTCACCGCCTGCGCATCC
TCCAGCGCCCGCTCCTTCTGCCGCACAAGGCCCTGCAGACGCAGATTCTCGCCCTCGGCcTCCCCAAGCT
GGCCCTTCAGCTCCGAGCACCGCTCCTGAAGCTTCCGCTCCGACTGCTCCAGCTCGGAGAGCTCGGCCTC
GTAATTGTCCCGTAAGCGCTTGATGCGGCTCTCGGCAGCCTTCTCACTCTCCTCCTTGGCCAGCGCCATGT
CGGCCTCCAGCCGGTGAATGACCAGCTCAATCTCCTTGTCCCGGCCTTCCGGATTCTTCCCTCAGCTCC
TGTTCCCGGTTTACGACGCCACGCCTCCTCCTTCTGGTGCGGGCCGGCCTCCACGCCTGCCTCTCCAGCT
CCAGCTGCTGCTTCAGGGTATTCAGCTCCATCTGGCGGGCCTGCAGCGTGGCCA

13690.4

CAACTTATTACTTGAAATTATAATATAGCCTGTCCGTTTGCTGTTTCCAGGCTGTGATATATTTTCCTAGTGG
TTTGACTTTAAAAATAAATAAGGTTTAATTTTCTCCCC

13693.1

TGCAAGTCACGGGAGTTTATTTATTTAATTTTTTTTCCCCAGATGGAGACTCTGTGCGCCAGGCTGGAGTGCA
ATGGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCACAGCCTCCCGA
GTAGCTGGGATTACAGGTGCCCGCCACCACACCCAGCTAATTTTTATTTTTAGTAAAGACAGGGTTTCCC
CATGTTGGCCAGGCTGGTCTTGAACCTTGACCTCAGGTGATCCACCTGCCTCGGCCTCCCAAAGTGTTGG
GATTACAGGCGTGAGCTACCCGTGCCTGGCCAGCCACTGGAGTTTAAAGGACAGTCATGTTGGCTCCAGC
CTAAGGCGGCATTTTCCCCCATCAGAAAGCCCGCGGCTCCTGTACCTCAAATAGGGCACCTGTAAAGTCA
GTCAGTGAAGTCTCTGCTCTAACTGGCCACCCGGGGCCATTGGCNTCTGACACAGCCTTGCCAGGANGCC
TGCATCTGCAAAAGAAAAGTTCACTTCCTTTCCG

13694.1

CAGAGAATCTKAGAAAGATGTCGCGTTTTCTTTAATGAATGAGAGAAGCCCATTGTATCCCTGAATCATTG
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GACCTCTAGCTCGAGCGCGAGGGACCTCCCGCCGGGATGCCTGGGGAGCAGATGGACCCTACTGGAAGT
CAGTTGGATTACAGATTTCTCTCAGCAAGATACTCCTTGCTGATAATTGAAGATTCTCAGCCTGAAAGCCAG
GTTCTAGAGGATGATTCTGGTTCTCACTTCAGTATGCTATCTCGACACCTTCCTAATCTCCAGACGCACAAA
GAAATCCTGTGTTGGATGTTGNGTCCAATCCTTGAACAAACAGCTGGAGAAGAACGAGGAGACCGGTAAT
AGTGGGTTCAATGAACATTTGAAAGAAAACCAGGTTGCAGACCCTG

13694.2

GA CTGT CCTGAACAAGGGACCTCTGACCAGAGAGCTGCAGGAGATGCAGAGTGGTGGCAGGAGTGGAAG
CCAAAGAACACCCACCTTCCTCCCTTGAAGGAGTAGAGCAACCATCAGAAGATACTGTTTTATTGCTCTGGT
CAAACAAGTCTTCCTGAGTTGACAAAACCTCAGGCTCTGGTGA CTTCTGAATCTGCAGTCCACTTTCCATAA
GTTCTTGTGCAGACA ACTGTTCTTTTGCTTCCATAGCAGCAACAGATGCTTTGGGGCTAAAAGGCATGTCCT
CTGACCTTGCAGGTGGTGGATTTTGCTCTTTTACAACATGTACATCCTTACTGGGCTGTGCTGTCACAGGGA
TGTCTTGCTGGACTGTTCTGCTATGGGGATATCTTCGTTGGACTGTTCTTCATGCTTAATTGCAGTATTAG
CATCCACATCAGACAGCCTGGTATAACCAGAGTTGGTGGT TACTGATTGTAGCTGCTCTTTGTCCACTTCAT
ATGGCACAAGTATTTTCCTCAACATCCTGGCTCTGGGAAG

13695.1

GAAATGTATATTTAATCATTCTCTTGAACGATCAGA ACTCTRAAATCAGTTTTCTATAACARCATGTAATACAG
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TCTGTGTGTGCTTCATGGAAGGTATATGTTTGTTGCCTTAATTTGAATTGTGGCCAGGAAGGGTCTGGAGAT
CTAAATTCAGAGTAAGAAAACCTGAGCTAGAACTCAGGCATTTCTCTTACAGAACTTGGCTTGCAGGGTAGA
ATGAANGGAAAGAACTTAGAAGCTCAACAAGCTGAAGATAATCCCATCAGGCATTTCCCATAGGCCTTGCA
ACTCTGTTCACTGAGAGATGTTATCCTG

13695.2

AGTCTGGAGTGAGCAAACAAGAGCAAGAAACAARRAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGA
TAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGA ACTAGACAAGTGTGTTAAGAGTG
ATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGG
GAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGA
GGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCACAAATTAAGCTGTAGTATGTACCC
TAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATT
CACTTTTTATGATGCTTCCCAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCCAAGTTGAGAAAAAT
GATCATAATTTTAGCATAAACCAGCAATCGGCGACCCC

13697.1

TAGCTGTCTTCCTCACTCTTATGGCAATGACCCCATATCTTAATGGATTAAGATAATGAAAGTGTATTTCTTA
CACTCTGTATCTATCACCAGAAGCTGAGGTGATAGCCCGCTTGTCATTGTCATCCATATTCTGGGACTCAGG
CGGGAAC TTTCTGGAATATTGCCAGGGAGCATGGCAGAGGGGCACAGTGCATTCTGGGGGAATGCACATT
GGCTCAGCCTGGGTAATGAGTGATATACATTACCTCTGTTCACTCATTGCCCAGCACCAGTCACAAGG
CCCCACCAAATACCAGAGCCCAAGAAATGTAGTCCTGTTGATATGGTTTTGCTGTGTCCCAACCCAAATCTC
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13697.2

ATCATGAGGATGTTACCAAAGGGATGGTACTAAACCATTTGTATTCTGCTGTTTTCACACTGCTTTGAAGATA
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TCAGGAACTTACAGTCATGGTGGAAGGCAAAGGAGGAGCAAGGCATGTCTTACATGTCAGTAGGAGAGA
GAGCGAGAGCAGGAGAACCTGCCACTTATAAACCATTCAGATCTCATAACTCCCTATCATGAGAAAAACATG
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13699.1&2

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13703.3

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ACAGTCA

13705.1

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13705.2

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13707.4

TCCCGCGCTCGCAGGGCNCGTGCCACCTGCCYGTCCGCCCCTCGCTCGCTCGCCCCGCCGCGCCGCGC
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CCGCTGCTGCCGCTGCTGCTGCTGC

13708.1&2

GGCGGGTAGGCATGGAAGTGAAGAAGCAAGAAGCTTTCAGACTACGTGGGGAAGAATGAAAAACCAA
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13709.1

TCTGAAGGTAAATGTTTCATCTAAATAGGGATAATGRTAAACACCTATAGCATAGAGTTGTTTGAGATTAA
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GTGGGANGGTAG

13709.2

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13712.1&2

TGAGGGACTGATTGGTTTGCTCTCTGCTATTCAATCCCCAAGCCCACTTGTTCCCTGCAGCGTCCTCCTTCT
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GTCTTGTTGAAGAGCTCATTCCACCAGTGGTTTGTGAACTCCTTGGCAGGGTCATGTCCTACCCCATGAGT
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13714.1&2

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TGCTC

13716.1&2

TTGGAATTAAATAAACCTGGAACAGGGAAGGTGAAAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGT
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13718.2

AAACTGGACCTGCAACAGGGACATGAATTTACTGCARGGTCTGAGCAAGCTCAGCCCCTCTACCTCAGGGC
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GACCCTGAACCAGAACCCAGCTGAACTGCCCCCTCCAAGGGACAGGAAGGCTGGGGGAGGGAGTTTACAA
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13722.3

CATGCGTTTCACCACTGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGCAATCCACCCGCCTCAGCCT
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CCGAGACTGCTTTTAATCCCAACTTCTCTACATTTAGATTAAAAAATATTTTATT.CATGGTCAATCTGGAACAT
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TAACCAAACATAAAATCATTAACTTTCAACTTAATAACTAATTGACATTCCTCAAAAGAGCTGTTTTCAAT
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13722.4

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AGAGTTGGGAGAATCTT

13724-13698-13748

GCCTACAACATCCAGAAAGAGTCTACCCTGCACCTGGTGCTSCGTCTCAGAGGTGGGATGCAGATCTTCGT
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ATAAAGTTGTTGCATTCCC

13730.1

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13732.1

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13732.2

ATAGGGGCTTTAAGGAGGGAATTCAGGTTCAATGAGGTCGTAAGGCCAGGGCTCTTATCCAGTAAGACTGG
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CCCAGGCAGAGTCATTCATCACGGCATCTCCTGAGCTAAACCAGCACCTGCTCTGCTCACTTCTTGACTGG
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13735.1

GGATAATGAAGTTGTTTTATTTAGCTTGGACAAAAAGGCATATTCCTCTATTTTCTTATACAACAAATATCCCC
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13735.2

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GGAAGTAAATAGGTTGATATTCAAGAGAGCACCTGAAGGCCAGGCGTGGTGGCTCACGCCTGTGGTCTAA
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13736.1

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GTGGGTACAAAGCC

13737.1&2

CAAATATTTAATATAAATCTTTGAAACAAGTTCAGAKGAAATAAAAATCAAAGTTTGCAAAAACGTGAAGATTA
ACTTAATTGTCAAATATTCCTCATTGCCCAAATCAGTATTTTTTTTATTTCTATGCAAAAGTATGCCTTCAA
CTGCTTAAATGATATATGATATGATACACAAACCAGTTTTCAAATAGTAAAGCCAGTCATCTTGCAATTGTAA
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CAATAATTTTTCGCTCCCACTTCTGCTGCTGTCTTCCACATCCTCACATAGACCCAGACCCGCTGGCCC
CTGGCTGGGCATCGCATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTACAGAAGCGATACACC
AAATTGCCTGGTTCGGTCATTGTCATAACCAG

"REPLACEMENT SHEETS"

13738.1

TTTGACTTTAGTAGGGGTCTGAACTATTTATTTTACTTTGCCMGTAATATTTARACCYTATATATCTTTTCATTA
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GGTTTCTGACCAGBGTGAGTTA

13738.2

AGAGAAGCCCCATAAATGCAATCAGTGTGGGAAGGCCTTCAGTCAGAGCTCAAGCCTTTTCCTCCATCATC
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13739.1&2

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13741.1

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13742.1

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14351.1

ACTCTGTCGCCCAGGCTGGAGCCCBATGGMGCGATCTCGACTCCCTGCAAGCTMCGCCTCACAGGWTCA
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T

14351.2

ACCTTAAAGACATAGGAGAATTTATACTGGGAGAGAAAGCTTACAAATGTAAGGTTTCTGACAAGACTTGGG
AGTGATTCACACCTGGAACAACATACTGGACTTCACACTGGABAGAAACCTTACAAGTGTAATGAGTGTGGC
AAAGCCTTTGGCAAGCAGTCAACACTTATTCACCATCAGGCAATTCA

14354.2

AGTCAGGATCATGATGGCTCAGTTTCCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTG
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14354.1

CTTTCGATTTCTTCAATTTGTCACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTATTATAGCT
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16431.1.2

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16432-1

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16432-2

GATGGCATGGTCGTTGCTAATGTGCCTGCTGGGATGGAGCACTTCCTCCTGTGAGCCCAGGGGACCCGCC
TGTCCCTGGAGCTTGGGGCAAGGAGGGAAGAGTGATACCAGGAAGGTGGGGCTGCAGCCAGGGGCCAGA
GTCAGTTCAGGGAGTGGTCCTCGGCCCTCAAAGCTCCTCCGGGGACTGCTCAGGAGTGATGGTGCCCTGG
AGTTTGGCCCAACTTCCCTGGCCACCCTGGAAGGTGCCTGGCTGCTCCAGGCCTCTAGGCTGGGCTGATG
GGTTTCTCCAGGACACAAGTATCATTAAAGCCACCCTCTCCTCAGCTTGTGAGGCCGCACATGTGGGACAG
GCTGTGCTCACAACCCCTCGCCTGCCCTGCCCTCCATCAGGAGGAGCCAGTGGAACCTTCGGAAAGCTC
CCAGCATCTCAGCAGCCCTCAAAGTCGTCTGGGGCAAGCTCTGGTTCTCCTGACTGGAGGTCATCTGG
GCTTGGCCTGCTCTCTCTCGC

17184.3

TAAAAAGTGTAACAAAGGTTTATTTAGACTTTCTTCATGCCCCCAGATCCAGGATGTCTATGTAAACCGTTA
TCTTACAAAGAAAGCACAAATATTTGGTATAAACTAAGTCAGTGACTTGCTTAACTGAAATAGCGTCCATCAA
AAGTGGGTTTAAAGGTAAACTACCTGACGATATTGGCGGGGATCCTGCAGTTTGGACTGCTTGCCGGGTTT
GTCCAGGGTTCCGGGTCTGTTCTTGGCACTCATGGGGACAGGCATCCTGCTCGTCTGTGGGGCCCCGCTG
GAGCCCTTACGTGAAGCTGAAGGTATCGACCSTAGGGGGCTCTAGGGCAGTGGGACCTTCATCCGGAAC
ACAAGGGTCGGGGAGAGGCCTCTTGGGCTATGTGGG

17184.4

CAAGCGTTCCTTTATGGATGTAAATTCAAACAGTCATGCTGAGCCATCCCGGGCTGACAGTCACGTTWAAG
ACACTAGGTCGGGCGCCACAGTGCCACCCAAGGAGAAGAAGAATTTGGAATTTTCCATGAAGATGTACGG
AAATCTGATGTTGAATATGAAAATGGCCCCCAAATGGAATTCCAAAAGGTTACCACAGGGGCTGTAAGACCT
AGTGACCCTCCTAAGTGGGAAAAGAGGAATGGAGAATAGTATTTCTGATGCATCAAGAACATCAGAATATAAA
ACTGAGATCATAATGAAGGAAAATTCCATATCCAATATGAGTTTACTCAGAGACAGTAGAACTATTCCCAG
G

17185.1

TAGGAATAACAAATGTTTATTCAGAAATGGATAAGTAATACATAATCACCCCTTCATCTCTTAATGCCCCCTTCC
TCTCCTTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGGAGGAGGACACAGGACTAG
CCCACCACCTTCTCTTCCCGGTCTCCCAAGATGACTGCTTATAGAGTGGAGGAGGCAAACAGGTCCCCTCA
ATGTACCAGATGGTCACCTATAGCACCAAGCTCCAGATGGCCACGTGGTTGCAGCTGGACTCAATGAACTC
TGTGACAACCAGAAGATACCTGCTTTGGGATGAGAGGGAGGATAAAGCCATGCAGGGAGGATATTTACCAT
CCCTACCCTAAGCACAGTGCAAGCAGTGAGCCCCCGGCTCCCAGTACCTGAAAAACCAAGGCCTACTGNC
TTTTGGATGCTCTCTTGGGCCACG

17188.2

AAGCCTCCTGCCCTGGAAATCTGGAGCCCCCTTGAGCTGAGCTGGACGGGGCAGGGAGGGGCTGAGAGG
CAAGACCGTCTCCCTCCTGCTGCAGCTGCTTCCCCAGCAGCCACTGCTGGGCACAGCAGAAACGCCAGCA
GAGAAAATGGGAGCCGAGAGTCCTTAGCCCTGGAGCTGAGGCTGCCTCTGGGCTGACCCGCTGGCTGTA
CGTGGCCAGAACTGGGGTTGGCATCTGGCATCCATTTGAGGCCAGGGTGGAGGAAAGGGAGGCCAACAG
AGGAAAACCTATTCCTGCTGTGACAACACAGCCCTTGTCACGCAGCCTAAGTGCAGGGAGCGTGATGAA
GTCAGGCAGCCAGTCGGGGAGGACGAGGTAAGTGCAGCAGCAATGTCACCTTGTAGCCTATGCGCTCAATG
GCCCCGAGGGGGCAGCAACCCCCCGCACACGTGAGCCAACAGCAGTGCCTCTGCAGGCACCAAGAGAGCG
ATGATGGACTTGAGCGCCGTGTTT

17190.1

GTTTGGCAGAAGACATGTTTAATAACATTTTCATATTTAAAAAATACAGCAACAATTCTCTATCTGTCCACCAT
CTTGCCTTGCCCTTCCTGGGGCTGAGGCAGACAAAGGAAAGGTAATGAGGTTAGGGCCCCCAGGCGGGCT
AAGTGCTATTGGCCTGCTCCTGCTCAAAGAGAGCCATAGCCAGCTGGGCACGGCCCCCTAGCCCCTCCAG
GTTGCTGAGGCGGCAGCGGTGGTAGAGTTCTTCACTGAGCCGTGGGCTGCAGTCTCGCAGGGAGAACTTC
TGCACCAGCCCTGGCTCTACGGCCCCGAAAGAGGTGGAGCCCTGAGAACCGGAGGAAACATCCATCACCT
CCAGCCCCTCCAGGGCTTCCTCCTCTTCCCTGGCCTGCCAGTTCACCTGCCAGCCGGGCTCGGGCCGCCA
GGTAGTCAGCGTTGTAGAAGCAGCCCTCCGCAGAAGCCTGCCGGTCAAATCTCCCCGCTATAGGAGCCCC
CCGGGAGGGGTCAGCACC

17190.2

CAAGTTGAACGTCAGGCTTGGCAGAGGTGGAGTGTAGATGAAAACAAAGGTGTGATTATGAAGAGGATGTG
AGTCCTTTGGGTGTAGGAGAGAAAGGCTGTTGAGCTTCTATTTCAAGATACTTTTACCTGTGCAAAAAGCAC
ATTTTCCACCTCCTTCTCATGGCATTGTGTAAAGGTGAGTATGATTCTATTCCATCTGCATTTTAGAGGTGA
AGAATAACGTACAAGGGATTCAGTGATTAGCAAGGGACCCCTCACTAAGTGTTGATGGAGTTAGGACAGAG
CTCAGCTGTTTGAATCTCAGAGCCCAGGCAGCTGGAGCTGGGTAGGATCCTGGAGCTGGCACTAATGTGA
GGTGCATTCCCTCCAACCCAGGCTCAGATCCGGAACCTGACCGTGCTGACCCCCGAAGGGGAGGCAGGG
CTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTACACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACT
ACTTCACAGAGCAGC

17191.2&89.2

TGGCCTGGGCAGGATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTAT
GACCCCATCATTTCCCCAGAGGTCTCGGCCTCCTTTGGTGTTGAGCAGCTGCCCTGGAGGAGATCTGGC
CTCTCTGTGATTTCACTGTGCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCT
TTGCCCAGTGCAAGAAGGGGGTGCGTGTGGTGAAGTGTGCCCGTGGAGGGATCGTGGACGAAGGCGCCC
TGCTCCGGGGCCCTGCAGTCTGGCCAGTGTGCCGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCAC
GGGACCGGGCCTTGGTGGACCATGAGAATGTCATCAGCTGTCCCCACCTGGGTGCCAGCACCAAGGAGG
CTCAGAGCCGCTGTGGGGAGGAAATTGCTGTTGAGTTCGTGGACATGGTGAAGGGGAAATCTCTCACGGG
GGTTGTGAATGCCCAGGCCCTT

"REPLACEMENT SHEETS"

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCCACAGCGATGAATGG
AGGGCCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACC
TTCAGGAGGTTACATAACAGGTGATCAAGCCCGTACTTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTT
AGCTGAAATATGGGCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTA
TGAAACTCATCAAGTTAAAGTTGCAGGGCCAAACAGCTGCCTGTAGTCCTCCCTCCTATCATGAAACAACCCC
CTATGTTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCCAATCTGTCCATTCATCAGCCAT
TGCCTCCAGTTGCACCTATAGCAACACCCTTGCTTCTGCTACTTCAGGGACCAGTATTCCTCCCCTAATGA
TGCCTGCTCCCCTAGTGCCTTCTGTAGTACATCCTCATTACCAAATGGAAGTCCAGTCTCATTACGCCTT
TATCCATTCCCTATTCTTCTTCAACATTGCCTCATGCATCATCTTACAGCCTGATGATGGGAGGATTTGGTGG
TGCTAGTATCCAGAAGGCCAGTCTCTGATTGATTTAGGATCTAGTAGCTCAACTTCCTCAACTGCTTCCCT
CTCAGGGAACCTCACCTAAGACAGGGACCTCAGAGTGGGCAGTTCCTCAGCCTTCAAGATTAAAGTATCGGC
AAAAATTTAATAGTCTAGACAAAGGCATGAGCGGATACCTCTCAGGTTTTCAAGCTAGAAATGCCCTTCTTC
AGTCAAATCTCTCTCAAACCTCAGCTAGCTACTATTTGGACTCTGGCTGACATCGATGGTGACGGACAGTTGA
AAGCTGAAGAATTTATTCTGGCGATGCACCTCACTGACATGGCCAAAGCTGGACAGCCACTACCACTGACG
TTGCCTCCCGAGCTTGTCCCTCCATCTTTCAGAGGGGGAAAGCAAGTTGATTCTGTTAATGGAAGTCTGCCT
TCATATCAGAAAACACAAGAAGAAGAGCCTCAGAAGAACTGCCAGTTACTTTTGAGGACAAACGGAAAGC
CAACTATGAACGAGGAAACATGGAGCTGGAGAAGCGACGCCAAGTGTTGATGGAGCAGCAGCAGAGGGA
GGCTGAACGCAAAGCCCAGAAAGAGAAGGAAGAGTGGGAGCGGAAACAGAGAGAACTGCAAGAGCAAGA
ATGGAAGAAGCAGCTGGAGTTGGAGAAACGCTTGGAGAAACAGAGAGAGCTGGAGAGACAGCGGGAGGA
AGAGAGGAGAAAGGAGATAGAAAGACGAGAGGCAGCAAAACAGGAGCTTGAGAGACAACGCCGTTTAGAA
TGGGAAAGACTCCGTCGGCAGGAGCTGCTCAGTCAGAAGACCAGGGAACAAGAAGACATTGTCAGGCTGA
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CTACAAGATGTCCAAATCAGAAAGCAAACACAAAAGACTGAGCTAGAAGTTTTGGATAAACAGTGTGACCTG
GAAATTATGGAAATCAAACAACCTTCAACAAGAGCTTAAGGAATATCAAATAAGCTTATCTATCTGGTCCCTG
AGAAGCAGCTATTAAACGAAAGAATTAAAAACATGCAGCTCAGTAACACACCTGATTCAGGGATCAGTTTAC
TTCATAAAAAGTCATCAGAAAAGGAAGAATTATGCCAAAGACTTAAGAACAATTAGATGCTCTTGAAAAAGA
AACTGCATCTAAGCTCTCAGAAATGGATTCAATTAACAATCAGCTGAAGGAACTCAGAGAAAGCTATAATAC
ACAGCAGTTAGCCCTTGAACAACCTTCATAAAATCAAACGTGACAAATTGAAGGAAATCGAAAGAAAAAGATT
AGAGCAAAAAAAAAAAAAA

"REPLACEMENT SHEETS"

ATGGCAGTGACATTCACCATCATGGGAACCACTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCA
CCCAGTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCT
AAGGTGCCAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAAA
CTTTCTAACTTCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAA
ACTGGTGTTACCCAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAAACAGGATGT
GCTTTCCTTTGCCCATTTAGGGTTTCTTCTCTTTCCTTTCTCTTTATTAACCACTA

ATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATA
TGAACAAGATAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTTCATGTGAAGTAGACAAGTGTG
TTAAGAGTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTGTAATG
TTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCACAAATTAAGCTGTAG
TATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGT
CAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTG
AGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTCGGCGACACCGATTTTATAAATAAACTGAGCACCTT
CTTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTTCATCCGTGAATGGTCCAGGGAAGGACCTT
TCACCTTGAATATATGGCATTATGTCATCACAAGCTCTGAGGCTTCTCCTTTCCATCCTGCGTGGACAGCTA
AGACCTCAGTTTTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGCGCCCCCATCTCCGGGG
GAATGTCTGAAGACAATTTTGTTACCTCAATGAGGGAGTGGAGGAGGATACAGTGCTACTACCAACTAGTG
GATAAAGGCCAGGGATGCTGCTCAACCTCCTACCATGTACAGGACGTCTCCCCATTACAACCTACCCAATCC
GAAGTGTCAACTGTGTCAGGACTAAGAAACCCTGGTTTTGAGTAGAAAAGGGCCTGGAAAGAGGGGAGCC
AACAAATCTGTCTGCTTCCTCACATTAGTCATTGGCAAATAAGCATTCTGTCTCTTTGGCTGCTGCCTCAGC
ACAGAGAGCCGAGAACTCTATCGGGCACCAGGATAACATCTCTCAGTGAACAGAGTTGACAAGGCCTATGGG
AAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTCTAAGTTTCTTTCCCTTCATTCTACCCTGCAAGCCA
AGTTCTGTAAGAGAAATGCCTGAGTTCTAGCTCAGGTTTTCTTACTCTGAATTTAGATCTCCAGACCCTTCCT
GGCCACAATTCAAATTAAGGCAACAAACATATACCTTCCATGAAGCACACACAGACTTTTGAAAGCAAGGAC
AATGACTGCTTGAATTGAGGCCTTGAGGAATGAAGCTTTGAAGGAAAAGAATACTTTGTTTCCAGCCCCCTT
CCCACACTCTTCATGTGTTAACCCTGCCTTCCTGGACCTTGAGGCCACGGTGACTGTATTACATGTTGTTA
TAGAAAATGATTTTAGAGTTCTGATCGTTCAAGAGAATGATTAAATATACATTTCTTA

Element Display											
Diff Exp	Exp	Probe 1	Probe 2	GEM/Element	Plate/Well	Probe 1	S/B	A%	Probe 2	S/B	A%
+1.7	384A Ovary T (nets)		272A Dendritic cells	42240608 (420)	421G0196 (C:11)	2393	13.7	50	1430	2.0	50
-1.1	335A Ovary T		S7 Ovary N	42220626 (420)	421G0196 (C:11)	355	2.7	54	362	1.8	54
+1.8	261A Ovary T		S10 Skeletal muscle N	42230621 (420)	421G0196 (C:11)	1288	6.9	51	707	1.9	51
+8.1	264A Ovary T		S2 Pancreas N	422N0629 (420)	421G0196 (C:11)	8590	44.1	62	1190	2.3	62
-1.2	386A Ovary T		S40 P BMC (activated)	422J0605 (420)	421G0196 (C:11)	516	3.8	50	619	2.0	50
+4.7	265A Ovary T		CT5 Heart N	42200624 (420)	421G0196 (C:11)	2305	14.1	53	489	2.2	53
-1.4	S25 Ovary T		CT4 Bone Marrow N	422H0619 (420)	421G0196 (C:11)	531	3.5	53	743	2.0	53
	383A Ovary T (nets)		I1 Colon N	422B0609 (420)	421G0196 (C:11)	1842	10.1	39	671	2.0	39
-1.9	S22 Ovary T		CT9 Kidney N	42290627 (420)	421G0196 (C:11)	453	3.3	66	657	3.2	66
+3.2	9485 OT 1-P (SCID)		9485 OT 5-P (SCID)	422Y0602 (420)	421G0196 (C:11)	1882	12.1	57	594	2.3	57
+1.5	262A Ovary T		334A Large Intestine N	422A0622 (420)	421G0196 (C:11)	1486	7.5	55	965	2.2	55
-1.1	S115 Ovary T (nets)		CT10 Small Intestine N	422C0604 (420)	421G0196 (C:11)	509	3.4	51	573	2.0	51
+1.1	288A Ovary T		CT12 Lung N	422V0625 (420)	421G0196 (C:11)	700	4.5	54	651	2.1	54
-2.1	201A Ovary T		S6 Stomach N	422V0620 (420)	421G0196 (C:11)	625	4.6	46	1335	3.6	46
+7.8	S23 Ovary T		S56 Spinal Cord N	422G0628 (420)	421G0196 (C:11)	3896	22.1	50	502	2.2	50
+1.8	205A Ovary T		270A Liver N	422Q0606 (420)	421G0196 (C:11)	2251	14.7	46	1256	2.0	46
-1.9	9334 Ovary T (SCID)		I2 Skin N	422R0601 (420)	421G0196 (C:11)	552	3.4	72	1029	2.3	72
+5.6	385A Ovary T		S91 Fetal tissue	422X0607 (420)	421G0196 (C:11)	6126	35.1	50	1449	2.0	50
-3.5	263A Ovary T		S73 Breast N	422H0623 (420)	421G0196 (C:11)	439	3.2	61	1531	3.4	61
-3.3	382A Ovary T		CT19 Brain N	422Q0610 (420)	421G0196 (C:11)	387	3.2	50	1278	2.1	50
+4.8	268A Ovary T		S27 Ovary N	422S0603 (420)	421G0196 (C:11)	4242	22.1	58	883	2.0	58

Fig. 3

Serial No. 09/827,271 Docket No. 210121.462C6

Inventor(s): Jennifer L. Mitcham et al.

Express Mail No. EV719392064US

"REPLACEMENT SHEETS"

TCGAGCGGCCGCCCCGGGCAGGTCCTTCAGACTTGGACTGTGTCACTGCCAGGCTTCCAGGGCTCCAAC
TTGCAGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACA
CCATGGTTTTATCCACCCTGAGATCTTTGAACAACCTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTG
GATATTTCTACCTCGGCCGCGACCACGCT

Fig. 4

Serial No. 09/827,271 Docket No. 210121.462C6

Inventor(s): Jennifer L. Mitcham et al.

Express Mail No. EV719392064US

"REPLACEMENT SHEETS"

TAGCGYGGTCGCGGCCGAGGYCTGCTTYTCTGTCCAGCCCAGGGCCTGTGGGGTCAGGGCGGTGGGTGC
AGATGGCATCCACTCCGGTGGCTTCCCCATCTTTCTCTGGCCTGAGCAAGGTCAGCCTGCAGCCAGAGTA
CAGAGGGCCAACACTGGTGTTCCTTGAACAAGGGCCTTAGCAGGCCCTGAAGGRCCCTCTCTGTAGTGTTG
AACTTCCTGGAGCCAGGCCACATGTTCTCCTCATACCGCAGGYTAGYGATGGTGAAGTTGAGGGTGAAATA
GTATTMANGRAGATGGCTGGCARACCTGCCCCGGCGGCCGCTCSAAATCC

Fig. 5

"REPLACEMENT SHEETS"

AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTCAGCTCT
CTGTACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTG
TCTGCACCCATCGTCCTGACCCCAAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCA
GCTGACCCACGGCATCACTGAGCTGGGCCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTC
ACCCATCGGAGCTCTGTACCCACCACCAGCACCGGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCCGGG
CGGCCGCTCGA

Fig. 7A

TTGGGGNTTTTMGAGCGGCCGCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACTT
CACCATCAACAACCTGCGGTATGAGGAGAACATGCAGCACCTGGCTCCAGGAAGTTCAACACCACGGAG
AGGGTCCTTCAGGGCCTGCTCAGGTCCCTGTTCAAGAGCACCAAGTGTGGCCCTCTGTACTCTGGCTGCA
GACTGACTTTGCTCAGACTTGAGAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCT
TGATCCCACTGGTCCTGGACTGGACAGAGAGCGGCTATACTGGGAGCTGAGCCAGTCCTCTGGCGGNGAC
NCCNCTT

Fig. 7B

AGCGTGGTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCCACTGGCACAGTGAGGAAGATC
TCTGCTGTCAGTGAGAAGGCTGTCATCCACTGAGATGGCAGTCAAAAGTGCAATTAATACACCTAACGTATC
GAACATCATAGCTTGCCCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCCCG
GGCGGCCGCTCGA

Fig. 7A and 7B

"REPLACEMENT SHEETS"

TGTGGTGTGAACTTCCTGGAGNCAGGGTGACCCATGTCCTCCCCATACTGCAGGTTGGTGATGGTGAAGT
TGAGGGTGAATGGTACCAGGAGAGGGCCAGCAGCCATAATTGTSGRGCKGSMGMSSGAGGMWGGWGT
YCWGAGGTTCYRARRTCCACTGTGGAGGTCCCAGGAGTGCTGGTGGTGGGCACAGAGSTCYGATGGGTG
AAACCATTGACATAGAGACTGTTCTGTCCAGGGTGTAGGGGCCAGCTCTTYRATGYCATTGGYCAGTTK
GCTYAGCTCCCAGTACAGCCRCTCTCKGYGGMGWCCAGSGCTTTTGGGGTCAAGATGATGGATGCAGATG
GCATCCACTCCAGTGGCTGCTCCATCCTTCTCGGACCTGAGAGAGGTCAGTCTGCAGCCAGAGTACAGAG
GGCCAACACTGGTGTCTTTGAATA

Serial No. 09/827,271 Docket No. 210121.462C6

Inventor(s): Jennifer L. Mitcham et al.

Express Mail No. EV719392064US

"REPLACEMENT SHEETS"

TCGAGCGGCCGCCCCGGGCAGGTCAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCACCTGT
GCTGCGGACATCTCCAGGGAGTGCAGAAGGGAAGCAGGTCAAAGTCTCAGATCAGTCAGACTGGCTGTT
CTCAGTTCTCACCTGAGCAAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTCTTGAACAA
GGGCTTGAGCAGACCCTGCAGAACCCTCTTCCGTGGTGTGAACTTCCTGGAAACCAGGGTGTGTCATGTT
TTTCCTCATAATGCAAGGTTGGTGATGG

Fig. 9

Gene Name	Bal Probe 1 Exp Name	P1	P2 Name	Probe 2 ID	GEM	Probe1 Value	Probe2 Value	Probe1 S/B	Probe2 S/B	Probe1 A%	Probe2 A%
42100188 (D3)	+7.0 205A Ovary T	42100188 (D3)	270A Liver N	422Q0606		8620	1240	57.7	2.2	65	65
42100188 (D3)	+5.9 S23 Ovary T	42100188 (D3)	S56 Spinal Cord N	422G0628		5894	1002	35.3	3.9	89	89
42100188 (D3)	+5.7 385A Ovary T	42100188 (D3)	S91 Fetal tissue	422X0607		12151	2121	54.3	7.3	73	73
42100188 (D3)	+5.1 426A Ovary T (met)	42100188 (D3)	415A Aorta N	422X0611		7487	1480	53.0	9.7	73	73
42100188 (D3)	+3.5 263A Ovary T	42100188 (D3)	S73 Breast N	422H0623		7302	2116	39.2	84	4.5	84
42100188 (D3)	+3.3 383A Ovary T (met)	42100188 (D3)	I1 Colon N	422B0609		3714	1113	20.4	83	2.6	83
42100188 (D3)	+3.0 933A Ovary T (SCII)	42100188 (D3)	I2 Skin N	422R0601		2435	814	12.1	75	2.1	75
42100188 (D3)	+2.6 384A Ovary T (met)	42100188 (D3)	272A Dendritic cell	422A0608		4578	1754	25.0	2.3	69	69
42100188 (D3)	+2.2 264A Ovary T	42100188 (D3)	S2 Pancreas N	422N0629		7904	3596	38.5	81	5.6	81
42100188 (D3)	+2.0 386A Ovary T	42100188 (D3)	S40 PB MC (activated)	422J0605		2191	1081	14.0	90	2.9	90
42100188 (D3)	+2.0 S115 Ovary T (met)	42100188 (D3)	CT10 Small intestine	422C0604		1979	971	10.4	80	2.7	80
42100188 (D3)	+2.0 265A Ovary T	42100188 (D3)	CT5 Heart N	422O0624		1911	964	13.9	93	3.4	93
42100188 (D3)	+2.0 335A Ovary T	42100188 (D3)	S7 Ovary N	42220626		1666	817	9.8	100	3.0	100
42100188 (D3)	-1.9 428A Ovary T (met)	42100188 (D3)	243A Esophagus N	422A0612		1827	3480	13.4	97	9.5	97
42100188 (D3)	+1.6 261A Ovary T	42100188 (D3)	S10 Skeletal muscle	42230621		5914	3653	30.4	86	6.0	86
42100188 (D3)	+1.6 266A Ovary T	42100188 (D3)	S27 Ovary N	42250603		2039	1274	11.9	50	2.6	50
42100188 (D3)	+1.6 S22 Ovary T	42100188 (D3)	CT9 Kidney N	42290627		1736	1072	11.0	92	4.0	92
42100188 (D3)	+1.4 9485 OT 1-P (SCID)	42100188 (D3)	9485 OT 5-P (SCID)	422Y0602		4204	3074	23.0	93	7.7	93
42100188 (D3)	+1.4 262A Ovary T	42100188 (D3)	334A Large Intestine	422A0622		3002	2101	16.6	89	4.0	89
42100188 (D3)	+1.3 S25 Ovary T	42100188 (D3)	CT4 Bone Marrow	422H0619		1643	1297	9.6	90	3.1	90
42100188 (D3)	+1.2 429A Ovary T (met)	42100188 (D3)	364A Ovary N	422I0614		2521	2084	22.0	65	23.9	65
42100188 (D3)	+1.2 382A Ovary T	42100188 (D3)	CT19 Brain N	422Q0610		2072	1663	10.9	88	2.3	88
42100188 (D3)	+1.2 288A Ovary T	42100188 (D3)	CT12 Lung N	422V0625		1840	1473	10.7	87	3.8	87
42100188 (D3)	+1.1 201A Ovary T	42100188 (D3)	S6 Stomach N	422W0620		1329	1204	9.1	90	3.5	90

Fig. 10

Gene Name	Bal Probe 1		Probe 2		GSM ID	Probe1		Probe2	
	Exp Name	P1	P2	Name		Value	S/B	Value	S/B
421B0181 [C3]	+18.8 385A Ovary T	Ⓢ	Ⓢ	S91 Fetal tissue	422X0607	26711	103.3	1424	2.0
421B0181 [C3]	+11.5 S23 Ovary T	Ⓢ	Ⓢ	S56 Spinal Cord N	422G0628	13559	65.3	1179	3.9
421B0181 [C3]	+11.1 426A Ovary T (mets)	Ⓢ	Ⓢ	415A Aorta N	422X0611	14125	67.3	1273	5.6
421B0181 [C3]	+10.8 205A Ovary T	Ⓢ	Ⓢ	270A Liver N	422Q0606	16121	93.1	1488	2.3
421B0181 [C3]	+5.1 263A Ovary T	Ⓢ	Ⓢ	S73 Breast N	422H0623	11326	58.2	2235	4.4
421B0181 [C3]	+4.6 384A Ovary T (mets)	Ⓢ	Ⓢ	272A Dendritic cells	42240608	6583	1424	24.5	2.1
421B0181 [C3]	+4.4 264A Ovary T	Ⓢ	Ⓢ	S2 Pancreas N	422N0629	9865	40.9	2245	3.6
421B0181 [C3]	+4.4 429A Ovary T (mets)	Ⓢ	Ⓢ	364A Ovary N	422I0614	2803	22.6	638	7.4
421B0181 [C3]	+4.2 261A Ovary T	Ⓢ	Ⓢ	S10 Skeletal muscle M	42230621	8271	39.5	1949	3.6
421B0181 [C3]	+3.8 S115 Ovary T (mets)	Ⓢ	Ⓢ	CT10 Small Intestine M	422C0604	2281	11.6	607	2.1
421B0181 [C3]	+2.5 265A Ovary T	Ⓢ	Ⓢ	CT5 Heart N	422O0624	3192	19.2	1293	4.0
421B0181 [C3]	-2.3 S22 Ovary T	Ⓢ	Ⓢ	CT9 Kidney N	42290627	565	3.6	1276	3.9
421B0181 [C3]	+2.2 266A Ovary T	Ⓢ	Ⓢ	S27 Ovary N	42250603	2774	14.3	1260	2.7
421B0181 [C3]	+2.1 9334 Ovary T (SCID)	Ⓢ	Ⓢ	I2 Skin N	422R0601	1774	8.4	837	2.1
421B0181 [C3]	+1.9 9485 OT 1-P (SCID)	Ⓢ	Ⓢ	9485 OT 5-P (SCID)	422Y0602	6967	41.5	3726	9.2
421B0181 [C3]	+1.6 382A Ovary T	Ⓢ	Ⓢ	CT19 Brain N	422Q0610	2313	6.2	1471	1.9
421B0181 [C3]	+1.6 288A Ovary T	Ⓢ	Ⓢ	CT12 Lung N	422V0625	1657	9.7	1054	2.9
421B0181 [C3]	-1.5 S25 Ovary T	Ⓢ	Ⓢ	CT4 Bone Marrow N	422H0619	848	4.5	1243	2.7
421B0181 [C3]	+1.4 262A Ovary T	Ⓢ	Ⓢ	334A Large Intestine	422A0622	3171	16.8	2214	3.8
421B0181 [C3]	+1.2 386A Ovary T	Ⓢ	Ⓢ	S40 PBMC (activated)	422I0605	630	4.2	544	1.9
421B0181 [C3]	-1.2 335A Ovary T	Ⓢ	Ⓢ	S7 Ovary N	42220626	592	3.7	730	2.6
421B0181 [C3]	-1.0 201A Ovary T	Ⓢ	Ⓢ	S6 Stomach N	422W0620	1197	7.8	1237	3.5
421B0181 [C3]	-1.0 428A Ovary T (mets)	Ⓢ	Ⓢ	243A Esophagus N	42240612	783	4.5	797	2.4
421B0181 [C3]	383A Ovary T (mets)	Ⓢ	Ⓢ	I1 Colon N	422B0609	3470	8.9	862	1.7

Fig. 11

Gene Name	Bal. Probe 1 Exp. Name	P1	P2 Name	GEM ID	Probe1 Value	Probe2 Value	Probe1 S/B	Probe1 A%	Probe2 S/B	Probe2 A%
42110182 (H7)	+16.7 426A Ovary T (met)	415A Aorta N	422X0611	7706	462	46.3	75	3.5	75	
42110182 (H7)	+10.7 205A Ovary T	270A Liver N	422Q0606	10171	950	61.2	41	1.8	41	
42110182 (H7)	+9.9 385A Ovary T	S91 Fetal tissue	422X0607	14415	1459	62.1	48	2.2	48	
42110182 (H7)	+8.8 523 Ovary T	S56 Spinal Cord N	422G0628	7781	880	47.3	73	3.4	73	
42110182 (H7)	+6.4 383A Ovary T (met)	I1 Colon N	422B0609	4807	748	27.6	47	2.2	47	
42110182 (H7)	+5.1 263A Ovary T	S73 Breast N	422H0623	9815	1909	57.1	74	4.2	74	
42110182 (H7)	+4.9 429A Ovary T (met)	364A Ovary N	422I0614	2661	543	20.3	61	6.7	61	
42110182 (H7)	+3.5 264A Ovary T	S2 Pancreas N	422N0629	7934	2274	38.8	71	3.9	71	
42110182 (H7)	-2.9 525 Ovary T	CT4 Bone Marrow	422H0619	480	1375	3.5	80	3.0	80	
42110182 (H7)	+2.8 261A Ovary T	S10 Skeletal muscle	42230621	8993	3245	34.6	69	5.1	69	
42110182 (H7)	+2.5 5115 Ovary T (met)	CT10 Small intestine	422C0604	1864	738	8.1	67	2.2	67	
42110182 (H7)	+2.3 9334 Ovary T (SCIT)	I2 Skin N	422R0601	2552	1113	12.7	41	2.6	41	
42110182 (H7)	-2.3 522 Ovary T	CT9 Kidney N	42290627	386	889	3.2	69	3.4	69	
42110182 (H7)	+2.2 384A Ovary T (met)	272A Dendritic cell	42240608	3516	1567	18.7	55	2.2	55	
42110182 (H7)	-2.2 382A Ovary T	CT19 Brain N	422Q0610	608	1320	4.2	60	2.3	60	
42110182 (H7)	+1.9 265A Ovary T	CT5 Heart N	422O0624	2063	1080	13.6	87	3.5	87	
42110182 (H7)	+1.8 266A Ovary T	S27 Ovary N	42250603	1550	847	7.0	58	2.1	58	
42110182 (H7)	+1.5 262A Ovary T	334A Large intestine	422A0622	2559	1651	13.2	73	3.2	73	
42110182 (H7)	-1.4 386A Ovary T	S40 PBMC (activated)	422I0605	534	738	3.9	62	2.2	62	
42110182 (H7)	-1.3 288A Ovary T	CT12 Lung N	422V0625	893	1120	5.3	66	3.1	66	
42110182 (H7)	-1.3 335A Ovary T	S7 Ovary N	42220626	440	567	3.3	60	2.2	60	
42110182 (H7)	+1.2 9485 OT 1-P (SCID)	9485 OT 5-P (SCID)	422Y0602	4188	3529	21.6	66	9.5	66	
42110182 (H7)	+1.1 428A Ovary T (met)	243A Esophagus N	42240612	725	689	6.2	65	2.8	65	
42110182 (H7)	-1.0 201A Ovary T	S6 Stomach N	422W0620	1008	1018	7.4	62	3.2	62	

Fig. 12

Gene Name	Bal Probe 1		Probe 2		GEM		Probe1		Probe2	
	Exp Name	P1	P2 Name	ID	Value	Value	S/B	A%	S/B	A%
421V0189 (D1)	+33.2 426A Ovary T (met)	421V0189 (D1)	415A Aorta N	422X0611	8072	243	55.2	67	2.4	67
421V0189 (D1)	+13.7 523 Ovary T	421V0189 (D1)	S56 Spinal Cord N	422G0628	7367	537	42.6	69	2.5	69
421V0189 (D1)	+12.6 429A Ovary T (met)	421V0189 (D1)	364A Ovary N	422I0614	2850	227	21.7	64	3.5	64
421V0189 (D1)	+8.0 385A Ovary T	421V0189 (D1)	S91 Fetal tissue	422X0607	11711	1469	54.0	58	2.2	58
421V0189 (D1)	+7.3 263A Ovary T	421V0189 (D1)	S73 Breast N	422H0623	6949	952	37.8	69	2.6	69
421V0189 (D1)	-5.8 525 Ovary T	421V0189 (D1)	CT4 Bone Marrow	422H0619	208	1210	2.1	44	2.9	44
421V0189 (D1)	+5.0 205A Ovary T	421V0189 (D1)	270A Liver N	422Q0606	8676	1737	52.3	57	2.6	57
421V0189 (D1)	+4.5 383A Ovary T (met)	421V0189 (D1)	I1 Colon N	422B0609	3149	707	17.4	57	2.0	57
421V0189 (D1)	+4.4 261A Ovary T	421V0189 (D1)	S10 Skeletal muscle	42230621	6332	1443	29.1	77	2.9	77
421V0189 (D1)	+4.2 264A Ovary T	421V0189 (D1)	S2 Pancreas N	422N0629	7612	1809	38.1	79	3.3	79
421V0189 (D1)	-3.2 382A Ovary T	421V0189 (D1)	CT19 Brain N	422Q0610	468	1508	3.4	60	2.3	60
421V0189 (D1)	+2.9 9334 Ovary T (SCID)	421V0189 (D1)	I2 Skin N	422R0601	2500	860	12.3	51	2.1	51
421V0189 (D1)	+2.5 5115 Ovary T (met)	421V0189 (D1)	CT10 Small intestine	422C0604	1424	569	6.7	61	2.1	61
421V0189 (D1)	+2.4 265A Ovary T	421V0189 (D1)	CT5 Heart N	422O0624	1742	723	11.8	70	2.8	70
421V0189 (D1)	+2.3 384A Ovary T (met)	421V0189 (D1)	272A Dendritic cell	42240608	3083	1342	17.0	62	2.0	62
421V0189 (D1)	+1.9 266A Ovary T	421V0189 (D1)	S27 Ovary N	42250603	1370	732	8.0	47	2.0	47
421V0189 (D1)	-1.9 386A Ovary T	421V0189 (D1)	S40 PBMC (activated)	422I0605	307	580	2.6	41	2.0	41
421V0189 (D1)	+1.7 262A Ovary T	421V0189 (D1)	334A Large Intestine	422A0622	2097	1202	11.2	86	2.7	86
421V0189 (D1)	-1.3 335A Ovary T	421V0189 (D1)	S7 Ovary N	42220626	373	470	2.9	47	2.0	47
421V0189 (D1)	-1.1 288A Ovary T	421V0189 (D1)	CT12 Lung N	422V0625	909	1094	5.6	72	2.9	72
421V0189 (D1)	+1.1 201A Ovary T	421V0189 (D1)	S6 Stomach N	422W0620	750	672	5.6	62	2.4	62
421V0189 (D1)	+1.1 428A Ovary T (met)	421V0189 (D1)	243A Esophagus N	42240612	498	446	4.2	73	2.1	73
421V0189 (D1)	-1.0 9485 OT 1-P (SCID)	421V0189 (D1)	9485 OT 5-P (SCID)	422Y0602	3117	3174	16.7	91	8.2	91
421V0189 (D1)	S22 Ovary T	421V0189 (D1)	CT19 Kidney N	42290627	224	409	2.3	48	2.3	48

Fig. 13

Gene Name	Expt Name	P1	P2 Name	Probe 2	GEM ID	Probe1 Value	Probe2 Value	Probe1 S/B	Probe1 A%	Probe2 S/B	Probe2 A%
421H0187 (E11)	+20.2 426A Ovary T (met)	+	415A Aorta N	415A Aorta N	422X0611	5441	270	36.3	50	2.3	50
421H0187 (E11)	+10.0 523 Ovary T	+	556 Spinal Cord N	556 Spinal Cord N	422G0628	5318	533	27.1	56	2.3	56
421H0187 (E11)	+8.3 420A Ovary T (met)	+	364A Ovary N	364A Ovary N	422I0614	1252	150	10.1	58	2.5	58
421H0187 (E11)	+5.7 385A Ovary T	+	S91 Fetal tissue	422X0607	9507	1668	35.8		45	2.1	45
421H0187 (E11)	+4.4 205A Ovary T	+	270A Liver N	422Q0606	3456	1235	31.1		50	2.0	50
421H0187 (E11)	+4.2 265A Ovary T	+	CT5 Heart N	422O0624	1834	438	11.9		48	2.0	48
421H0187 (E11)	-4.1 382A Ovary T	-	CT19 Brain N	422Q0610	309	1259	2.6		48	2.0	48
421H0187 (E11)	+3.6 261A Ovary T	+	S10 Skeletal muscle	422J0621	3733	1036	17.7		55	2.3	55
421H0187 (E11)	+3.4 263A Ovary T	+	S73 Breast N	422H0623	4163	1239	23.0		62	3.0	62
421H0187 (E11)	+2.5 S115 Ovary T (met)	+	CT10 Small intestine	422C0604	1565	627	8.8		47	2.1	47
421H0187 (E11)	+2.1 264A Ovary T	+	S2 Pancreas N	422N0629	3455	1630	14.9		60	3.0	60
421H0187 (E11)	+2.1 384A Ovary T (met)	+	272A Dendritic cell	422A0608	2667	1270	13.4		44	1.9	44
421H0187 (E11)	-2.1 S22 Ovary T	-	CT9 Kidney N	42290627	291	605	2.4		51	2.5	51
421H0187 (E11)	-1.7 386A Ovary T	-	S40 PBMC (activated)	422J0605	410	687	3.2		47	2.0	47
421H0187 (E11)	+1.6 933A Ovary T (SCII)	+	I2 Skin N	422R0601	1622	984	7.9		44	2.2	44
421H0187 (E11)	+1.5 262A Ovary T	+	334A Large Intestine	422A0622	1892	1245	10.1		50	2.6	50
421H0187 (E11)	-1.5 288A Ovary T	-	CT12 Lung N	422Y0625	604	908	4.1		62	2.6	62
421H0187 (E11)	-1.4 428A Ovary T (met)	-	243A Esophagus	N42240612	236	325	2.7		78	1.9	78
421H0187 (E11)	-1.3 335A Ovary T	-	S7 Ovary N	42220636	382	501	2.9		58	2.0	58
421H0187 (E11)	-1.2 201A Ovary T	-	S6 Stomach N	422W0620	558	677	4.2		58	2.3	58
421H0187 (E11)	+1.0 9485 OT 1-P (SCID)	+	9485 OT 5-P (SCID)	422Y0602	2582	2493	15.1		57	6.3	57
421H0187 (E11)	383A Ovary T (met)	+	J1 Colon N	422B0609	2261	562	12.5		38	1.7	38
421H0187 (E11)	266A Ovary T	+	S27 Ovary N	42250603	1739	965	9.7		36	2.2	36
421H0187 (E11)	S25 Ovary T	+	CT4 Bone Marrow	422H0619	283	845	2.2		44	2.2	44

Fig. 14

11721-1

ACGGTTTCAATGGACACTTTTATTGTTTACTTAATGGATCATCAATTTTGTCTCACTACCTACAAATGGAATTT
CATCTTGTTTCCATGCTGAGTAGTGAAACAGTGACAAAGCTAATCATAATAACCTACATCAAAAGAGAACTAA
GCTAACACTGCTCACTTTCTTTTAAACAGGCCAAAATATAAATATATGCACTCTAXAATGCACAATGGTTTAGT
CACTAAAAAATTCAAATGGGATCTTGAAGAATGTATGCAAATCCAGGGTGCAGTGAAGATGAGCTGAGATG
CTGTGCAACTGTTTAAGGGTTCCTGGCACTGCATCTCTTGCCACTAGCTGAATCTTGACATGGAAGGTTTT
AGCTAATGCCAAGTGGAGATGCAGAAAATGCTAAGTTGACTTAGGGGCTGTGCACAGGAAGCTAAAAGGCAG
GAAAGTACTAAATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAGCTCCAAACTGGCA
CCACCCCAGTGCTCACATGGCTGACTTTATCCTCCGTGTTCCATTTGGCACAGCAAGTGGCAGTG

11721-2

AAGGCTGGTGGGTTTTTGATCCTGCTGGAGAACCTCCGCTTTCATGTGGAGGAAGAAGGGAAGGGAAAAG
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GGGGATGTCTATGTCAATGATGCTTTTGGCACTGCTCACAGAGCCACAGCTCCATGGTAGGAGTCAATCT
GCCACAGAAGGCTGGTGGGTTTTTGATGAAGAAGGAGCTGAACTACTTTGCAAAGGCCTTGAGAGCCCA
GAGCGACCCTTCCTGGCCATCCTGGGCGGAGCTAAAGTTGCAGACAAGATCCAGCTCATCAATAATATGCT
GGACAAAGTCAATGAGATGATTATTGGTGGTGGAAATGGCTTTTACCTTCCTTAAGGTGCTCAACAACATGGA
GATTGGCACTTCTCTGTTTGATGAAGAGGGAGCCAAGATTGTCAAAGACCTAATGTCCAAAGCTGAGAAGA
ATGGTGTGAAGATTACCTTGCCTGTTGACTTTGTCACTGCTGACAAGTTTGATGA

11724-1

TTTGTTCTTACATTTTTCTAAAGAGTTACTTAAATCAGTCAACTGGTCTTTGAGACTCTTAAGTTCTGATTCC
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TTTTCCCCCTGTAGAGTATCACAGACCTTCTGCTGAAGCTGGACCTCTGTCTGGGCCTTGACTCCCAAAT
CTGCTTGTCATGTTCAAGCCTGGAAATGTTAATCTTTAATTCTTCCATATGGATGGACATCTGTCTAAGTTGA
TCCTTTAGAACACTGCAATTATCTTCTTTGAGTCTAATTTCTTCTTTGCTTTGAATCGCATCACTAAACTT
CCTCTCCCATTTCTTAGCTTCATCTATCACCTGTACGATCATCCTGGAGGGAAGACATGCTCTTAGTAAA
GGCTGCAAGCTGGGTACAGTACTGTCCAAGTTTTCTGAAGTTGCTGAACTTCCTTGTCTTTCTTGTTCAA
AGTAACCTGAATCTCTCCAATTGTCTCTTCCAAGTGGACTTTTTCTCTGCGCAAAGCATCCAG

11724-2

TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTCAATCAATCAAAGGATT
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ACAAGAAGGAGACAGAAAAGCAGTTGCAGGAAGCTGAGCAAGAAATGGAGGAAATGAAAGAAAAGATGAG
AAAGTTTGCTAAATCTAAACAGCAGAAAATCCTAGAGCTGGAAGAAGAGAATGACCGGCTTAGGGCAGAGG
TGCACCCTGCAGGAGATACAGCTAAAGAGTGTATGGAAACACTTCTTCTTCCAATGCCAGCATGAAGGAA
GAACTTGAAAGGGTCAAAATGGAGTATGAAACCCTTTCTAAGAAGTTTCAGTCTTTAATGTCTGAGAAAGAC
TCTCTAAGTGAAGAGGTTCAAGATTTAAAGCATCAGATAGAAGGTAATGTATCTAAACAAGCTAACCTAGAG
GCCACCGAGAAACATGATAACCAAACGAATGTCACTGAAGAGGGAACACAGTCTATACCAGGT

11725-32-1.2

AAGCCAATAATCACCATTTATTACTTAATATATGCCAACCCTGTACTTGGCAGTTCACAAATTCTCACCGTT
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GAGCCAAGTATACACAGAATACGAAGTGGCAAACTAGAAGGAAAGACTGACACTGCTATCTGCTGGCCTC
CAGTGTCTGGCTCTTTTCACACGGGTCAATGTCTCCAGCGCTGCTGCTGCTGCTGCATTACCATGCCCTC
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GAAAGATCACTCTCCCTCTCTTTTAGCATGGCTTCTAACCTCTTCAATTCATTTTCTTTTCAACACAAT
CTCAAGTTCTTCAAAGTGTGATGCAGAAGAGGCCTCTTTCAAGTTATGTTGTGCTACTTCCTGAACATGTGC
TTTTAAAGATTCATTTTCTTCTTGAAGATCCTGTAACCACTTCCCTGTATTGGCTAGGTCTTTCTTTCTCTT
CCAAAACAGCCTTCATGGTATTCATCTGTTCTCTTTTCTTTTAATAAGTTCAGGAGCTTCAGAAC

11726-1&2

CAAGCTTTTTTTTTTTTTTAAAAAGTGTTAGCATTAAATGTTTTATTGTCACGCAGATGGCAACTGGGTTTATG
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CCTGAAAAGCAGTCTTGCTCTCGATCTGCTTACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGG
ACCGATGGAAATGGATCCAAAGCACCAACAGAGCTTCAAGACTCGCTGCTTGGCTTGAATTCGGATCCGA
TATCGCCATGGCT

11727-1&2

AAGTGTTAGCATTAAATGTTTTATTGTCACGCAGATGGCAACTGGGTTTATGTCTTCATATTTTATATTTTGT
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11728.1.40.19.19

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TCAGCACAACAGACGCCCTGGCGGTAGGGACAGCAGGCCAGCCCTGTCGGTTGTCTCGGCAGCAGGTC
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AAG

11728.2.40.19.19

CCCGTGGGTGCCATCCACGGAGTTGTTACCTGATCTTTGGAAGCAGGATCGCCCGTCTGCACTGCAGTGG
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GTCCCTGAGACGGTAAAGATGCAGGAGTGGCCGGCAGAGCAGTGGGCATCAACCTGGCAGGGGCCACCC
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GGTCCAGGCAGCAGGCCACAGGGCAGAACTGACCATCTGGGCACCGCGTTCCAGCCACCAGCCCTGCTG
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CCGATCACCTGCACTGCTGCCCAAGACACTGTGTGTGACCTGATCCAGAGTAAGTGCCTCTCCAAGGAGA
ACG

11730-1

GAATCACCTTTCTGGTTTAGCTAGTACTTTGTACAGAACAATGAGGTTTCCCACAGCGGAGTCTCCCTGGGC
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GACATTATGCATTGTGCTCACATTCCCTTAAATGTTGTTTCCAAAGGTGCTCAGCCTCTAGCCCAGCTGGAT
TCTCCGGGAAGAGGCAGAGACAGTTTGGCGAAAAAGACACAGGGAAGGAGGGGGTGGTGAAAGGAGAAA
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GGGTCAGAGGGAGGAGCAGCAGCAGGGTGGGACTGGGGCGT

11730-2

AACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGC
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11732.1contig

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11732.2contig

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11735-1-2

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11740.2.contig

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11765.2&64.2.contig

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11767.2.contig

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11768-1&2

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11768-1&2-11735-1&2

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11769.1.contig

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11769.2.contig

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11770.1.contig

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11770.2.contig

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11773.1.contig

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11778.1.contig

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11778-2&30-2

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11782.1.contig

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11782.2.contig

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11783-1 & 2

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11786.1.contig

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11786.2.contig

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13691.1&2

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13692.1&2

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13693.2

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13696.1-13744.1

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13700.1

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13700.2

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13701.1

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"REPLACEMENT SHEETS"

13701.2

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13702.2

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13704.2-13740.2

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13706.1

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13706.2

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13707.3

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13710.2

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13710-1

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13711.1

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13711.2

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13713.1&2

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13715.4

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13717.1&2

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13719.1&2

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13721.1

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13721.2

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13723.1

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13723.2

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13725.1

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13725.2

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13726.1&2

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AAAT

13727.1

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13727.2

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13728.1&2

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13731.1&2

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13734.1&2

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ACTT

13736.2

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13744.2-13696.2

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13746.1&2-13720.1&2

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14347.1

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GT

14347.2

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14348.2&14350.1&2

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GAAGGC

14349.1&2

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Express Mail No. EV719392064US

"REPLACEMENT SHEETS"

14352.182

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14353.1

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14353.2

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17182.18&2

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AGCAGCTCAAGATCCTCAACCTCCGCTTCCTGGGGAAGCTCCTGGAAGCCTGAAGCAGGCAGGGCCGGTG
GACTTCGTGCGATGAAGAGTGATCCTCCTTCCTTCCCTGGCCCTTGGCTGTGACACAAGATCCTCCTGCAG
GGCTAGGCGGATTGTTCTGGATTTCTTTTGTTCCTTTTAGGTTTCCATCTTTTCCCTCCCTGGTGCTCA
TTGGAATCTGAGTAGAGTCTGGGGGAGGGTCCCCACCTTCCTGTACCTCCTCCCCACAGCTTGCTTTTGT
GTACCGTCTTTCAATAAAAAGAAGCTGTTTGGTCTA

"REPLACEMENT SHEETS"

17183.2

GGTTCACAGCACTGCTGCTTGTGTGTTGCCGGCCAGGAATTCCAGGCTCACAAGGCTATCTTAGCAGCTCG
TTCTCCGGTTTTTAGTGCCATGTTTGAACATGAAATGGAGGAGAGCAAAAAGAATCGAGTTGAAATCAATGA
TGTGGAGCCTGAAGTTTTTAAGGAAATGATGTGCTTCATTTACACGGGGAAGGCTCCAAACCTCGACAAAAT
GGCTGATGATTTGCTGGCAGCTGCTGACAAGTATGCCCTGGAGCGCTTAAAGGTCATGTGTGAGGATGCC
CTCTGCAGTAACCTGTCCGTGGAGAACGCTGCAGAAATTCTCATCCTGGCCGACCTCCACAGTGCAGATCA
GTTGAAAACCTCAGGCAGTGGATTTTCATCAACTATCATGCTTCGGATGTCTTGGAGACCTCTTGGG

17186.1&2

TCGTAGCCATTTTTCTGCTTCTTTGGAGAATGACGCCACACTGACTGCTCATTGTCGTTGGTTCCATGCCAA
TTGGTGAAATAGAACCTCATCCGGTAGTGAGCCGGAGGGACATCTTGTCAACGGTGATGGTGCGATT
TGGAGCATAACCAGAGCTTGGTGTCTCGCCATACAGGGCAAAGAGGTTGTGACAAAGAGGAGAGATACGG
CATGCCTGTGCAGCCCTGATGCACAGTTCCTCTGCTGTGTACTCTCCACTGCCAGCCGGAGGGGCTCCC
TGTCCGACAGATAGAAGATCACTTCCACCCCTGGCTTG

17187.1&2

TGGCACACTGCTCTTAAGAACTATGAWGATCTGAGATTTTTTTGTGTATGTTTTTACTCTTTTGAGTGGTA
ATCATATGTGTCTTTATAGATGTACATACCTCCTTGACAAATGGAGGGGAATTCATTTTCATCACTGGGAGT
GTCCTTAGTGTATAAAAACCATGCTGGTATATGGCTTCAAGTTGAAAAATGAAAGTGACTTTAAAAGAAAAT
AGGGGATGGTCCAGGATCTCCACTGATAAGACTGTTTTTAAGTAACTTAAGGACCTTTGGGTCTACAAGTAT
ATGTGAAAAAATGAGACTTACTGGGTGAGGAAATTCATTGTTTAAAGATGGTCGTGTGTGTGTGTGTGTGT
GTGTGTGTTGTGTTGTGTTTTGTTTTTAAGGGAGGGAATTTATTATTTACCGTTGCTTGAAATTACTGKGTA
AATATATGTYTGATAATGATTTGCTYTTTGVCMACTAAAATTAGGVCTGTATAAGTWCTARATGCMTCCTG
GGKGTGATYTTCCMAGATATTGATGATAMCCCTTAAAATTGTAACCYGCCTTTTTCCCTTTGCTYTCMATTA
AAGTCTATTCMAAAG

17191.1&89.1

GGGGGTAGGCTCTTTATTAGACGGTTATTGCTGTACTACAGGGTCAGAGTGCAGTGTAAAGCAGTGTGAGAG
GCCCCGCTTCAGCCCAAGAATGTGGATTTTCTCTCCCTATTGATCACAGTGGGTGGGTTTCTTCAGAAAAG
CCCCAGAGGCAGGGACCAAGTGAAGCTCCAAGGTTAGAAGTGGAAGTGGAAAGGCTTCAGTCACATGCTGCTT
CCACGCTTCCAGGCTGGGCAGCAAGGAGGAGATGCCCATGACGTGCCAGGTCTCCCCATCTGACACCAAGT
GAAGTCTGGTAGGACAGCAGCCGCACGCCTGCCTCTGCCAGGAGGCCAATCATGGTAGGCAGCATTGCAG
GGTCAGAGGTCTGAGTCCGGAATAGGAGCAGGGGCAGGTCCCTGCGGAGAGGCACTTCTGGCCTGAAGA
CAGCTCCATTGAGCCCCTGCAGTACAGGYGTAGTGCCTTGGACCAAGCCACAGCCTGGTAAGGGGGCGCC
TGCCAGGGCCACGGCCAGGAGGCA

"REPLACEMENT SHEETS"

17192.1&2

TAATTTCTTAGTCGTTTGGAAATCCTTAAGCATGCAAAAGCTTTGAACAGAAGGGTTCACAAAGGAACCAGGG
TTGTCTTATGGCATCCAGTTAAGCCAGAGCTGGGAATGCCTCTGGGTTCATCCACATCAGGAGCAGAAGCAC
TTGACTTGTGCGTCCTGCTGCCACGGTTTGGGCGCCACCACGCCACGTCCACCTCGTCCTCCCCTGCC
GCCACGTCCTGGGCGGCCAAGGTCTCCAAAATTGATCTCCAGCTGAGACGTTATATCATTTGCTGGCTTCC
GGAAATGATGGTCCATAACCGAATCTTCAGCATGAGCCTCTTCACTCTTTGATTTATGAAGAACAAATCCCTT
CTTCCACTGCCCATCAGCACCTTCATTTGGTTTTCGGATATTAAATTCTACTTTTGCCCGGTCTTATTTTGA
ATAGCCTTCCACTCATCCAAAGTCATCTCTTTTGACCCTCCTCTTTTACCTCTTCAACTTCATTCTCCTTATT
TTCAGTGTCTGCCACTGGATGATGTTCTTCACCTTCAGGTGTTTCCTCAGTCACATTTGATTGATCCAAGTCA
GTTAATTCGTCTTTGACAGTTCCCCAGTTGTGAGATCCGCTACCTCCACGTTTGTCTCGTGTTCAGGCCA
GATCTATCACTTCCACTATGCCTATCAAATTCACGTTTGCCACGAGAATCAAATCCATCTCCTCGGCCATT
CCACGTCCACGGCCCCCTCGACCTCTTCCAAGACCACCACGACCTCGAATAGGTGGTCAATAATCGGTCT
ATCAACTGAAAATTCGCCTCCTTCACCCTTTTCTTCAAGTGGCTTTTGAATCTTCGTTACGAGGTGGTCG
CCTTTCTGGTCTTCTATCAATTATTTCCCTTCACCCTGAAGTTGTTGATCAGGTCTTCTTCCAACCTCGTGC

17193

AAGCGGATGGACCTGAGTCAGCCGAATCCTAGCCCCCTTCCCTTGGGCCTGCTGTGGTGCTCGACATCAGT
GACAGACGGAAGCAGCAGACCATCAAGGCTACGGGAGGCCCGGGCGCTTGCGAAGATGAAGTTTGGCT
GCCTCTCCTTCCGGCAGCCTTATGCTGGCTTTGTCTTAAATGGAATCAAGACTGTGGAGACGCGCTGGCGT
CCTCTGCTGAGCAGCCAGCGGAAGTGTACCATCGCCGTCCACATTGCTCACAGGGACTGGGAAGGCGATG
CCTGTCGGGAGCTGCTGGTGGAGAGACTCGGGATGACTCCTGCTCAGATTCAGGCCTTGCTCAGGAAAGG
GGAAAAGTTTGGTCGAGGAGTGATAGCGGGACTCGTTGACATTGGGGAACTTTGCAATGCCCCGAAGAC
TTAACTCCCGATGAGGTTGTGGAAGTAGAAAATCAAGCTGCACTGACCAACCTGAAGCAGAAGTACCTGAC
TGTGATTTCAAACCCAGGTGGTTACTGGAGCCCATACCTAGGAAAGGAGGCAAGGATGTATTCCAGGTAG
ACATCCCAGAGCACCTGATCCCTTTGGGGCATGAAGTGTGACAAGTGTGGGCTCCTGAAAGGAATGTTCCR
GAGAAACCAGCTAAATCATGGCACCTTCAATTTGCCATCGTGACGCAGACCTGTATAAATTAGGTAAAGAT
GAATTTCCACTGCTTTGGAGAGTCCCACCCACTAAGCACTGTGCATGTAAACAGGTTTCTTTGCTCAGATGA
AGGAAGTAGGGGGTGGGGCTTTCTTGTGTGATGCCTCCTTAGGCACACAGGCAATGTCTCAAGTACTTTG
ACCTTAGGGTAGAAGGCAAAGCTGCCAGTAAATGTCTCAGCATTGCTGCTAATTTTGGTCTGCTAGTTTCT
GGATTGTACAAATAAATGTGTTGTAGATGA

Fig. 15U

16443.1.edit

TCGAGCGGCCGCCCCGGGCAGGTGTGCGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCT
GCCCATTGCTCTCCCACTCCACGGCGATGTGCTGGGATAGAAGCCTTTGACCAGGCAGGTCAGGCTGAC
CTGGTTCTTGGTCATCTCCTCCCGGGATGGGGGCAGGGTGTACACCTGTGGTTCTCGGGGCTGCCCTTTG
GCTTTGGAGATGGTTTTCTCGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTA CTCTT GCC
ATTCAACCAGTCCTGGTGCANGACGGTGAGGACGCTNACCACACGGTACGNGCTGGTGTACTGCTCCTCC
CGCGGCTTTGTCTTGGCATTATGCACCTCCACGCCGTCCACGTACCAATTGAACTTGACCTCAGGGTCTTC
GTGGCTCACGTCCACCACCACGCATGTAACTCAAANCTCGGNCGCGANACGC

16443.2.edit

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC
AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCC
CCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACC
TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA
CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACACCTGCCGGGCGGCCGCTCGA

16444.2.edit

AGCGTGGTTNCGGCCGAGGTCCCAACCAAGGCTGCANCCTGGATGCCATCAAAGTCTTCTGCAACATGGA
GACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAGCAAGAAC
CCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCC
AGGGCTCCGACCCTGCCGATGTGGACCTGCCCGGGCGGNCGCTCGA

16445.1.edit

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACT
GGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAAC
ATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAGCA
AGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG
CGGCCAGGGCTCCGACCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

16445.2.edit

TCGAGCGGTGCGCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAAT
CCATCGGNCATGCTCTCGCCGAACCAGACATGCCTCTTGNCCTTGGGGTTCTTGCTGATGTACCAGNTCTT
CTGGGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCANTCTCCATGTTGCANAAGACTTTGATG
GCATCCAGGTTGCAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGACAGAGTGGCACATCTT
GAGGTCACGGCAGGTGCGGGCGGGGTTCTTGACCTCGGTGCGGACCACGCT

16446.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCCTCCTCAGAGCGGTAGCTGTTCTTATTGCCCCGGCAGCCTCCATAGA
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GACTGCGTTGGCGGTGCAGTATTCTTCATAGTTGAACATATCGCTGGAGTGGACTTCAGAATCCTGCCTTCT
GGGAGCACTTGGGACAGAGGAATCCGCTGCATTCTGCTGGTGGACCTCGGCCGCGACCACGCT

16446.2.edit

AGCGTGGTCGCGGCCGAGGTCCACCAGCAGGAATGCAGCGGATTCTCTGTCCCAAGTGCTCCCAGAAG
GCAGGATTCTGAAGACCACTCCAGCGATATGTTCAACTATGAAGAATACTGCACCGCCAACGCAGTCACTG
GGCCTTGCCGTGCATCCTTCCCACGCTGGTACTTTGACGTGGAGAGGAACCTCCTGCAATAACTTCATCTAT
GGAGGCTGCCGGGGCAATAAGAACAGCTACCGCTCTGAGGAGGACCTGCCCGGGCGGCCGCTCGA

16447.1.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAAT
CCATCGGTCATGCTCTCGCCGAACCAGACATGCCTCTTGTCCTTGGGGTTCTTGCTGATGTACCAGTTCTT
CTGGGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATG
GCATCCAGGTTGCAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAATGGCACATCTT
GAGGTCACGGCANGTGCGGGCGGGGTTCTTGACCTCGGCCGCGACCACGCT

16447.2.edit

AGCGTGGTCGCGGGCCGAGGTCAAGAAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGG
CTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCA
ACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAG
CAAGAACCCCAAGGACAAGAGGCATGTCTGGCTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTAT
GGCGGCCAGGGCTCCGACCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

16449.1.edit

AGCGTGGTCGCGGGCCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGNTCCAGGAACCCTGAACTGTAAGG
GTTCTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGNAATGGGGCCCATGAN
ATGGTTGNCTGAGAGAGAGCTTCTTGTCTACATTGCGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGT
GGCCGTTGNGGGCGGTGNGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGT
GCTGACCANAAGTGCCAGGAAGCTGAATACCATTTCCAGTGTACATACCCAGGGTGGGTGACGAAAGGGGT
CTTTTGAAGTGTGGAAGGAACATCCAAGATCTCTGNTCCATGAAGATTGGGGTGTGGAAGGGTTACAGTT
GGGGAAGCTCGCTGTCTTTTCTTCCAATCANGGGCTCGCTCTTCTGAATATTCTTCAGGGCAATGACATA
AATTGTATATTCGGTTCCCGGTTCCAGGCCAG

16450.1.edit

TCGAGCGGGCCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCA
GGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCG
CCCTGGTGTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCC
TGAAGAATAATCAGAAGAGCGAGCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACC
CTTCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTTCGTC
ACCCACCCTGGGTATGACACTGGAAATGGTATTAGCTTCTGGCACTTCTGGTCAGCAACCCAGTGTGG
GCAACAAATGATCTTTGANGAACATGGNTTTAGGCGGACCACACCGGCCACAACGGGCACCCCCATAAGG
CATAGGCCAAGAACATACCCGNCGAATGTAGGACAAGAAGCTCTNTCTCANACAANCATCTCATGGGCCCC
ATTCCANGACACTTCTGAGTACATCANTTCATGGCATCCTGGTGGCACTGATAAAAACCCTTACAGTTA

16450.2.edit

AGCGTGGTCGCGGGCCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGTTCAGGAACCCTGAACTGTAAGG
GTTCTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAG
ATGGTTGTCTGAGAGAGAGCTTCTTGTCTACATTGCGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGT
GGCCGTTGTGGGCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGT
GCTGACCAGAAGTGCCAGGAAGCTGAATACCATTTCCAGTGTACATACCCAGGGTGGGTGACGAAAGGGGT
CTTTTGAAGTGTGGAAGGAACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACAGTT
GGGGAAGCTCGTCTGTCTTTTCTTCCAATCANGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACAT
AAATTGTATATTCGNTCCCGGGTNCAGCCAATAATAAACCTCTGTGACACCANGGCGGGGCCGAAGG
ANCACT

16451.1.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTACCACCTACAACATCATAGTGGAGGCACTGAAAGACC
AGCAGAGGCATAAGGTTCCGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACC
TACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGT
CTGAATCAGGCTTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTGAGATGTGATTCATCTA
GATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACC
TGCCCGGGCGGCCGCTCGA

16451.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACAC
CATTGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACA
GTTTAAAGCCTGATTCAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAA
AGCACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGNTGACAGAGTTGCCACGGTAACAACCTCTTCCCGA
ACCTTATGCCTCTGCTGGTCTTTCAGTGCCCTCCACTATGATGTTGTAGGTGGTACCTCTGGTGAGGACCTC
GGCCGCGACCACGCT

16452.1.edit

AGCGTGGCCGCGGCCGAGGTCCATTGGCTGGAACGGCATCAACTTGGAAGCCAGTGATCGTCTCAGCCTT
GGTTCTCCAGCTAATGGTGATGGNGGTCTCAGTAGCATCTGTACACGAGCCCTTCTTGGTGGGCTGACAT
TCTCCAGAGTGGTGACAACACCCTGAGCTGGTCTGCTTGTCAAAGTGTCTTAAGAGCATAGACACTCACT
TCATATTTGGCGNCCACCATAAGTCCTGATACAACCACGGAATGACCTGTCAGGAAC

16452.2.edit

TCGAGCGGCCGCCCCGGGCAGGTCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA
TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCTGACCAACTGACCTGAAGTTCA
CTCAGGTCACACCCACAAGCCTGAGCGCCAGTGGACACCACCCAATGTTTCAGCTCACTGGATATCGAGT
GCGGGTGACCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTG
GTTGTATCAGGACTTATGGCGGCCACCAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGC
AGACCAGCTCAGGGTGTGTCACCACTCTGGAGAATGTCAGCCCACCAAGAAGGGCTCGTGTGACAGATG
CTACTGAGACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCC
GTTCCAGCCAATGGACCTCGGCCGCGACCACGCTT

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16453.1.edit

AGCGTGGTCGCGGCCGAGGTCTGGCCGAAGTCCAGTGACAGGGAAGATGTACATGTTATAGNTCTTCT
CGAAGTCCCGGGGCCAGCAGCTCCACGGGGTGGTCTCCTGCCTCCAGGCGCTTCTCATTCTCATGGATCTT
CTTCACCCGCAGCTTCTGCTTCTCAGTCAGAAGGTTGTTGTCCTCATCCCTCTCATACAGGGTGACCAGGA
CGTTCTTGAGCCAGTCCCGCATGCGCAGGGGGGAATTCGGTCAGCTCAGAGTCCAGGCAAGGGGGGATGT
ATTTGCAAGGCCCGATGTAGTCCAAGTGGAGCTTGTGGCCCTTCTTGGTGCCCTCCAAGGTGCACTTTGTG
GCAAAGAAGTGGCAGGAAGAGTCGAAGGTCTTGTTGTCATTGCTGCACACCTTCTCAAACCTCGCCAATGGG
GGCTGGGCAGACCTGCCCCGGCGGCCGCTCGA

16453.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTGCCAGCCCCCATTGGCGAGTTTGAGAAGGNGTGCAGCAATGACA
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AAGCTCCACCTGGACTACATCGGGCCTTGCAAATACATCCCCCCTTGCCTGGACTCTGAGCTGACCGAATT
CCCCCTGCGCATGCGGGACTGGCTCAAGAACGTCTGGTCACCCTGTATGAGAGGGATGAGGACAACAAC
CTTCTGACTGAGAAGCANAAAGCTGCGGGTGAAGAAATCCATGAGAATGANAAGCGCCTGNAGGCANGAG
ACCACCCCGTGGAGCTGCTGGCCCCGGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACTGCTG
CAGTTCGGCCAGACCTCGGCCGCGACCACGCT

16454.1.edit

AGCGTGGNTGCGGACGACGCCCACAAAGCCATTGTATGTAGTTTTANTTCAGCTGCAAANAATACCNCCAG
CATCCACCTTACTAACCAGCATATGCAGACA

16454.2.edit

TCGAGCGGTGCCCCGGGCAGGTCTGGGCGGATAGCACCGGGCATATTTTGAATGGATGAGGTCTGGCA
CCCTGAGCAGCCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCACGGT
TCTGAGTCTGTGGGATAGCTGCCATGAAGNAACCTGAAGGAGGCGCTGGCTGGTANGGGTTGATTACAGG
GCTGGGAACAGCTCGTACACTTGCCATTCTCTGCATATACTGGNTAGTGAGGCGAGCCTGGCGCTCTTCTT
TGCGCTGAGCTAAAGCTACATACAATGGCTTTGNGGACCTCGGCCGCGACCACGCTT

16455.1.edit

TCGAGCGGCCGCCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACCTTCTCTCCAATCTTGTAGTTCACAC
CATTGTCATGACACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACA
GTTTAAAGCCTGATTGAGACATTGTTCCCACTCATCTCCAACGGCATAATGGGAAACTGTGTAGGGGTCAA
AGCACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAAGTTGCCCACGGTAACAACCTCTTCCCG
AACCTTATGCCTCTGCTGGTCTTTCAAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACC
TCGGCCGCGACACGCT

16455.2.edit

AGCGTGGTTTGCGGCCGAGGTCCTCACCANAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGAC
CAGCAGAGGCATAAGGTTCTGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAAC
CTACGGATGACTCGTGCTTTGACCCCTACACAGNTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATG
TCTGAATCAGGCTTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTGAGATGTGATTCATCT
ANATGGTGTGATGACAATGGTGNGAACTACAAGATTGGAGAGAAGTGGNACCGTCAGGGGANAAAATGGA
CCTGCCCGGGCGGCNCGCTCGA

16456.1.edit

AGCGTGGTTCGCGGCCGAGGTCTGGCTTNCTGCTCANGTGATTATCCTGAACCATCCAGGCCAAATAAGCG
CCGGCTATGCCCCTGNATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAG
ATTGATC

16456.2.edit

TCGAGCGGCCGCCCGGGCAGGTCCAATTGAAACAAACAGTTCTGAGACCGTTCTTCCACCACTGATTAAGA
GTGGGGNGGCGGGTATTAGGGATAATATTCATTTAGCCTTCTGAGCTTTCTGGGCAGACTTGGTGACCTTG
CCAGCTCCAGCAGCCTTCTGGTCCACTGCTTTGATGACACCCACCGCAACTGTCTGTCTCATATCACGAAC
AGCAAAGCGACCCAAAGGTGGATAGTCTGAGAAGCTCTCAACACACATGGGCTTGCCAGGAACCATATCAA
CAATGGGCAGCATCACCAGACTTCAAGAATTTAAGGGCCATCTTCCAGCTTTTTACCAGAACGGCGATCAAT
CTTTTCCTTCAGCTCAGCAAACCTTGCATGCAATGTGAGCCG

"REPLACEMENT SHEETS"

16459.1.edit

TCGAGCGGCCGCCCGGGCAGGTCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAA
TTGCTGGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTT
GTGGNTACTGACCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGC
GCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACT
CAGNGGGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTAAC
ACCCATGGGANGNCATGCCTGATCTGGACTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAACAGGCT
GNTTGCTGANAAAGCAAGTGACCAAGGANGAAATTCANGGGTGAAANGGACTGCTCCCGCTCCTGAATTC
ACTGCTACTCAACCTGANGNTGCAGACTGGTCTTGAAGGNGNACANGGGCCCTCTGGGCCTATTTAAGCA
NCTTCGGTCGCGAACACGNT

16459.2.edit

AGCGTGNGTCGCGGCCGAGGTGCTGAATAGGCACAGAGGGCACCTGTACACCTTCAGACCAGTCTGCAAC
CTCAGGCTGAGTAGCAGTGAACCTCAGGAGCGGGAGCAGTCCATTACCCCTGAAATTCCTCCTTGGNCACT
GCCTTCTCAGCAGCAGCCTGCTCTTCTTTTCAATCTCTTCAGGATCTCTGTAGAAGTACAGATCAGGCATG
ACCTCCCATGGGTGTTACGGGAAATGGTGCCACGCATGCGCAGAACTTCCCGAGCCAGCATCCACCACA
TCAAACCCACTGAGTGAGCTCCCTTGTTGTTGCATGGGATGGGCAATGTCCACATAGCGCAGAGGAGAATC
TGTGTTACACAGCGCAATGGTAGGTAGGTTAACATAAGATGCCTCCGCGAGAAGCTGGTGGTCAGCCCTG
GGGTCAAGTAACCACAAGAAGCCGTGGCTCCCGGAAGGCTGCCTGGATCTGGTTAGTGAAGGNTCCAGGA
GTGAAGCGGCCAACAATTGGAGTGGCTTCAGTGGAAGCAGCAAACTTCAGCACAAGCCCTCTGGACCTG
CCCGGCGGCCGCTCGA

16460.1.edit

TCGAGCGGCCGCCCGGGCAGGTCCATTTTCTCCCTGACGGNCCCACTTCTCTCCAATCTTGTAGTTCACAC
CATTGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACA
GTTTAAAGCCTGATTACAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAA
AGCACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCNTCCCCG
AACCTTATGCCTCTGCTGGGCTTTCAGNGCCTCCACTATGATGNTGTAGGGGGGCACCTCTGGNGANGAC
CTCGGCCGCGACCACGCT

16460.2.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACC
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TACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAATGT
CTGAATCAGGCTTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGGTCAATTCAGATGTGATTCATCT
AGATGGTGCCATGACAATGGNGNGAACTACAAGATTGGAGAGAAGTGGNACCGNCAGGGAGAAAATGGAC
CTGCCCGGGCGGCCGCTCGA

16461.1.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCC
ATCGGTCATGCTCTCGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTG
GGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCA
TCCAGGNTGCAACCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAGTGGCACATCTTGAG
GTCACGGCAGGTGCGGNCGGGGGNTTTTGGCGCTGCCCTCTGGNCTTCGGNTGTNCTCNATCTGCTGGC
TCA

16461.2.edit

TCGAGCGGCCGCCCGGGCAGGTCTCGCGGTGCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCT
CCTGGACCTCCTGGCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTC
AAGAGAAGGCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCTGTGACCGTGACCT
CGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGCAGNCG
CAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGG
ATTGACCCCAACCAAGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGC
GTGTACCCCACTCAGCCCAGTGTGGCCCAAAGAAGTGGTACATCAGCAAGAACCCCAAGGACAAGAAGC
ATGTCTGGTTCGGCGAGAACATGACCGATGGATTCCAGTTCGAGTATGGCGGGCAGGGCTCCGACCCTGC
CGATGGGGACCTTGGCCGCGAACACGCT

16463.1.edit

AGCGTGGNNGCGGCCGAGGTATAAATATCCAGNCCATATCCTCCCTCCACACGCTGANAGATGAAGCTGT
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16463.2.edit

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16464.1.edit

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16464.2.edit

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16465.1.edit

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16465.2.edit

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16466.2.edit

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16467.2.edit

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12_16474.edit

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13_16475.edit

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14_16475.edit

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16_16476.edit

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17_16477.edit

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18_16477.edit

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21_16479.edit

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22_16479.edit

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27_16482.edit

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29_16483.edit

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31_16484.edit

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"REPLACEMENT SHEETS"

38_16487.edit

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39_16488.edit

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41_16489.edit

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45_16491.edit

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46_16491.edit

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47_16492.edit

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48_16492.edit

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"REPLACEMENT SHEETS"

49_16493.edit

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55_16496.edit

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59_16498.edit

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61_16499.edit

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62_16483.edit

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"REPLACEMENT SHEETS"

63_16500.edit

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64_16493.edit

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64_16500.edit

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"REPLACEMENT SHEETS"

16501.edit

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16501.2.edit

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16502.1.edit

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16502.2.edit

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Fig. 15QQ

"REPLACEMENT SHEETS"

16503.1.edit

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16503.2.edit

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16504.2.edit

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16505.1.edit

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16505.2.edit

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16506.1.edit

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16506.2.edit

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16507.1.edit

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16507.2.edit

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16508.1.edit

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16508.2.edit

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"REPLACEMENT SHEETS"

16509.1.edit

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16510.1.edit

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16510.2.edit

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16511.2.edit

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16512.1.edit

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16512.2.edit

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"REPLACEMENT SHEETS"

16514.1.edit

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16514.2.edit

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"REPLACEMENT SHEETS"

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16519.2.edit

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16523.2.edit

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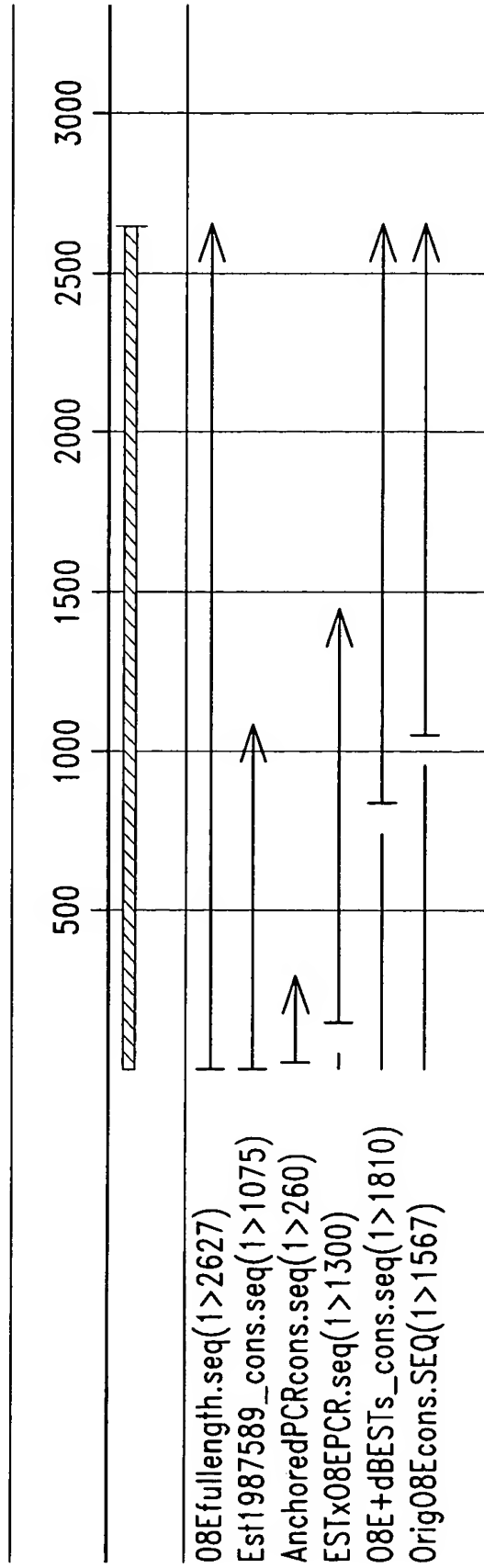


Fig. 16

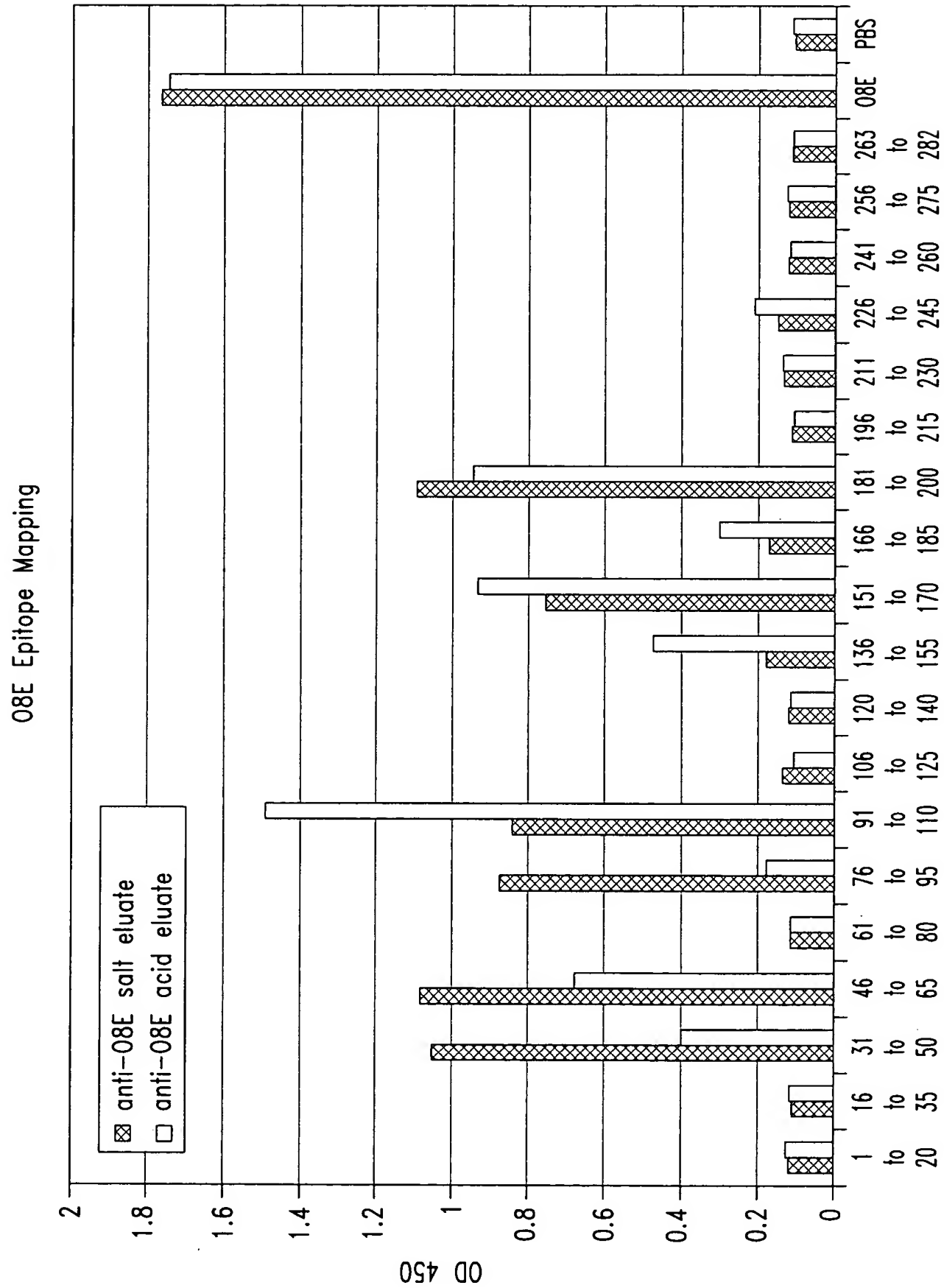


Fig. 17

O8E Surface Expression

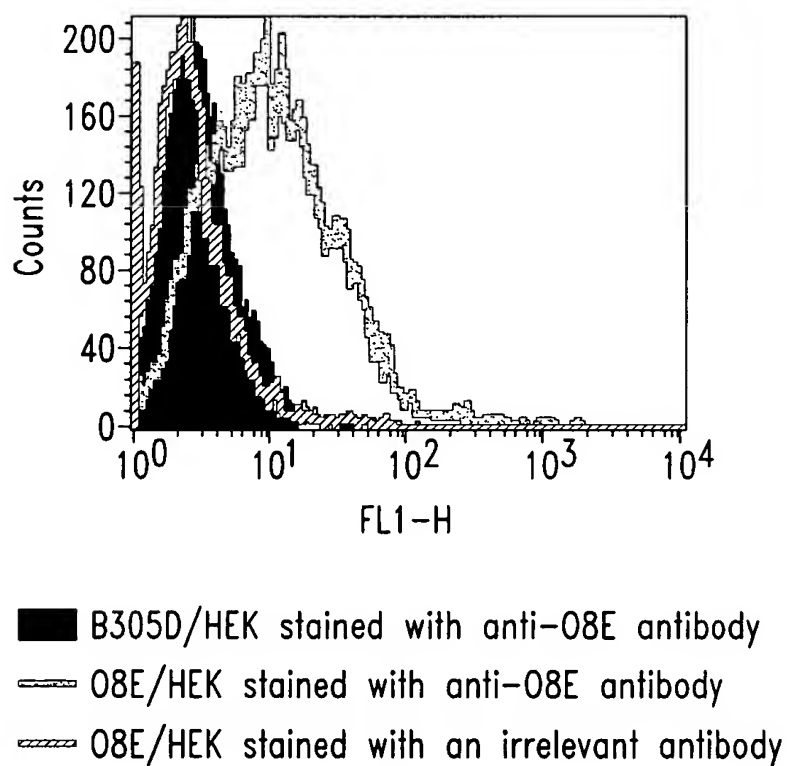


Fig. 18

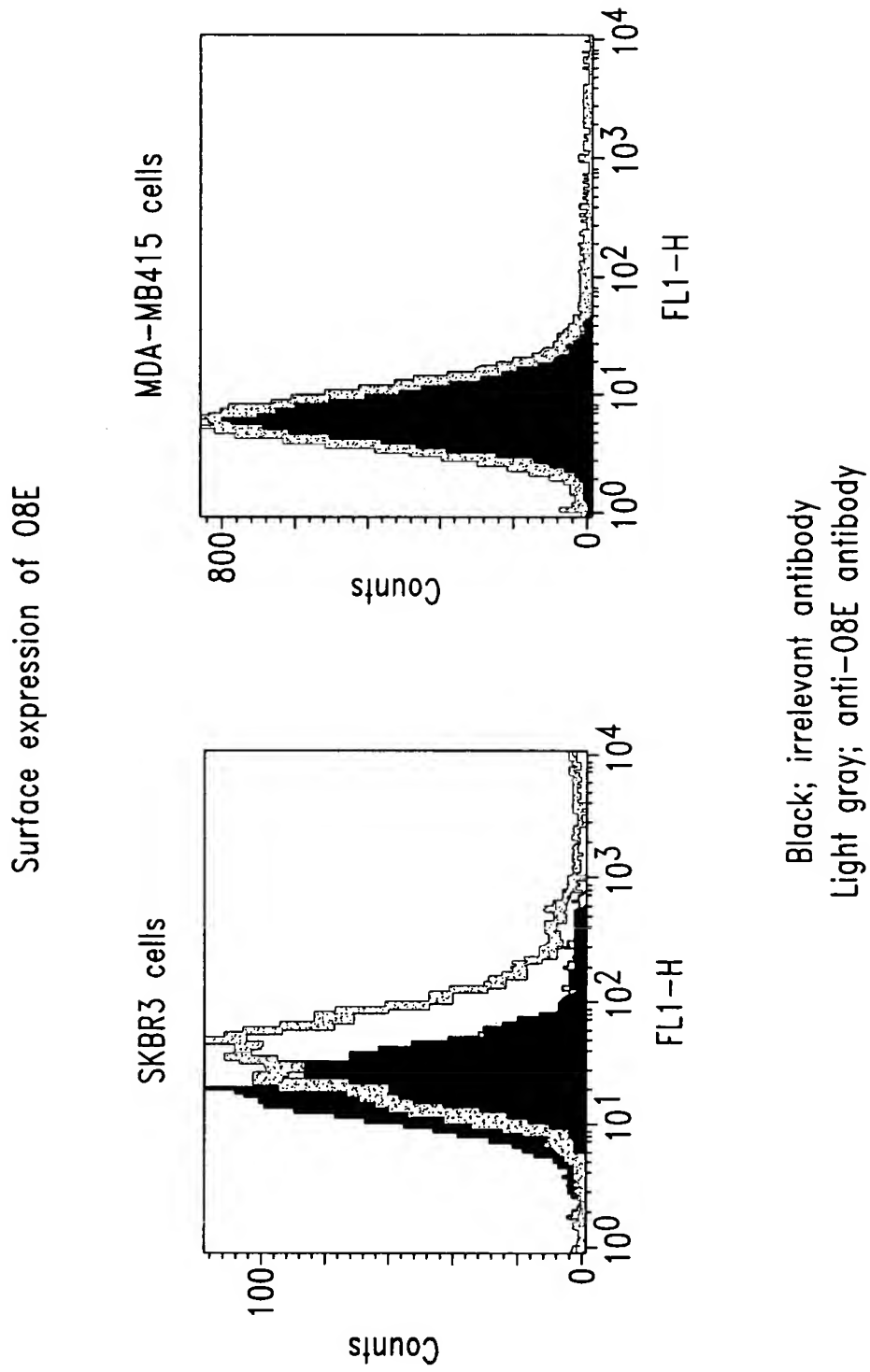


Fig. 19

O8E Surface Expression

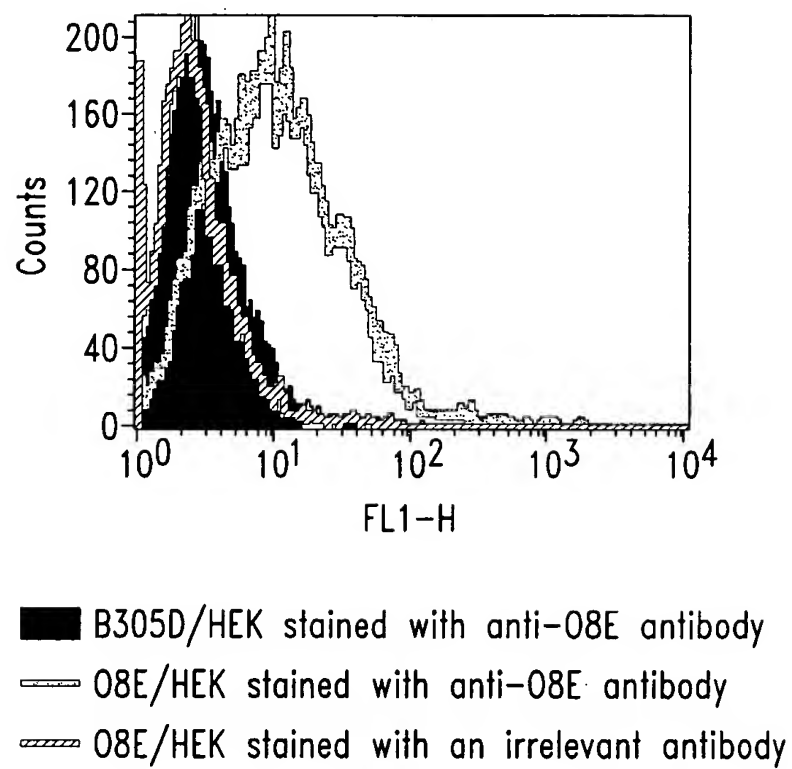


Fig. 20

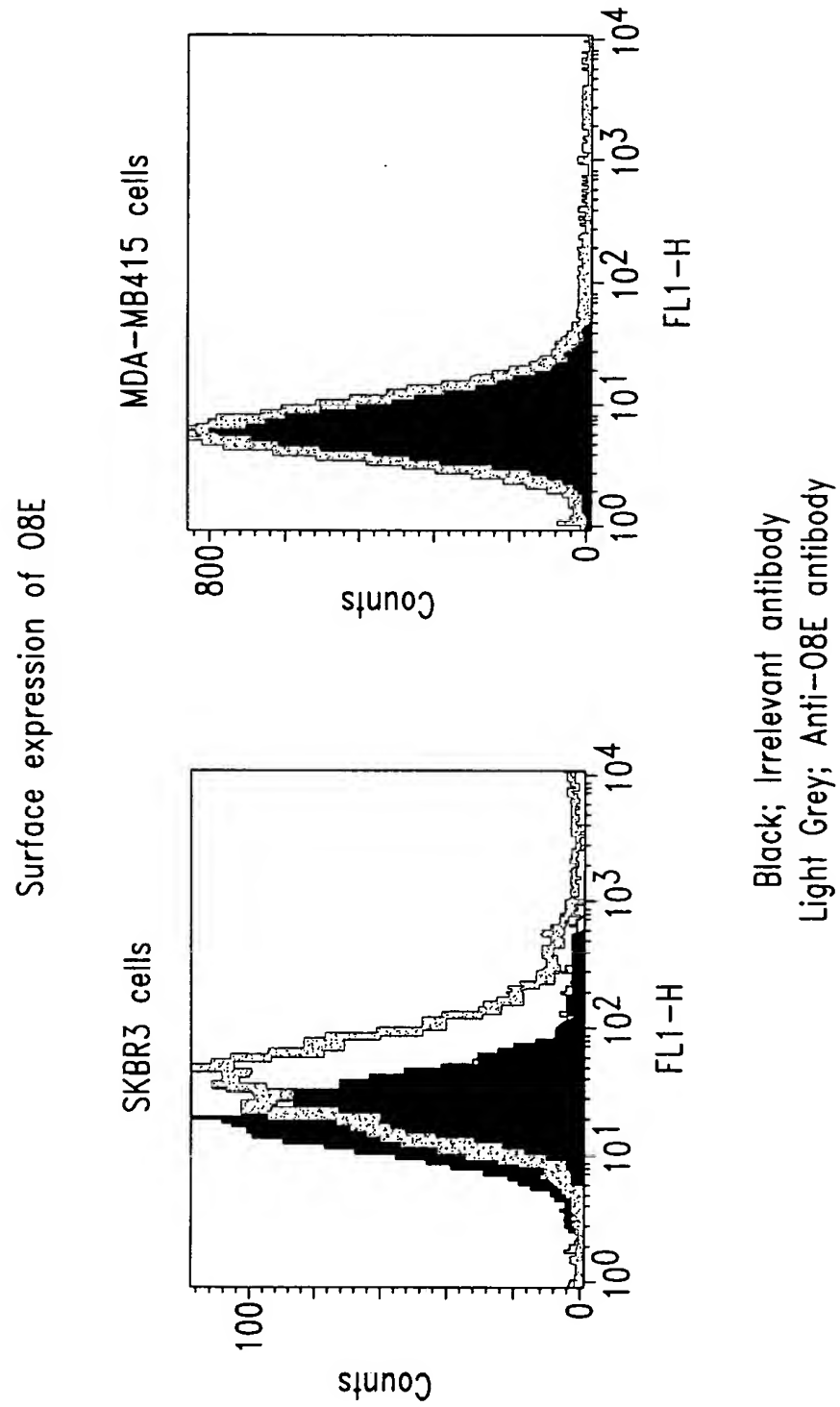


Fig. 21

O8E expression in HEK293 Cells
(probed with anti-O8E rabbit polyclonal sera #2333L)



Fig. 22

08E Rabbits 01212000

Date: 1/21/99

Antigen on Plate	Sera Sample	Antibody Dilutions											
		1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000
08E (#632-24)	Preimmune sera (#2576L):11/10/99	0.13	0.09	0.08	0.07	0.07	0.07	0.07	0.06	0.07	0.07	0.07	0.07
	Average	0.10	0.08	0.07	0.07	0.07	0.07	0.07	0.06	0.06	0.07	0.06	0.07
	α -08E (#2576K):1/11/2000	0.11	0.08	0.07	0.07	0.07	0.07	0.07	0.06	0.07	0.07	0.06	0.07
	Average	2.92	2.81	2.74	2.70	2.58	2.08	1.61	1.01	0.68	0.40	0.24	0.15
	Preimmune sera (#2333L):11/10/99	2.93	2.77	2.74	2.69	2.48	2.08	1.57	1.00	0.66	0.40	0.23	0.16
	Average	2.93	2.79	2.74	2.69	2.53	2.08	1.59	1.00	0.67	0.40	0.23	0.16
	Preimmune sera (#2333L):11/10/99	0.09	0.07	0.06	0.06	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	Average	0.08	0.07	0.06	0.07	0.10	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	α -08E (#2333L):1/11/2000	0.08	0.07	0.06	0.06	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	Average	2.73	2.75	2.64	2.48	2.30	1.78	1.41	0.92	0.58	0.32	0.20	0.14
	Preimmune sera (#2333L):1/11/2000	2.73	2.76	2.51	2.60	2.37	1.93	1.44	0.88	0.58	0.35	0.20	0.14
	Average	2.73	2.76	2.57	2.54	2.33	1.85	1.43	0.90	0.58	0.33	0.20	0.14

Fig. 23

affi-pure O8E #2576L 739.87A&B

Date: 5/2/2000	
Antibody Name	O8E polyclonal
Rabbit #, Bleed Date	2576L, 1/11/2000
Purification Method	affinity
Buffer	PBS
Notebook	#705, p150
lot #	739.87A
Antibody Concentration	1.4mg/ml
Initial Amount	18mg
	739.87B
	1.7mg/ml
	3mg

Antigen on Plate	Sera Sample	Antibody Dilutions													
		1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000		
#632-24	preimmune sera (2576L)	0.15	0.11	0.09	0.08	0.08	0.07	0.07	0.07	0.07	0.08	0.07	0.08	0.07	0.08
	Average	0.14	0.10	0.09	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	α -O8E (2576K):2/8/2000	2.74	2.71	2.63	2.49	2.29	1.87	1.39	0.92	0.57	0.33	0.20	0.14	0.20	0.14
	Average	2.72	2.68	2.64	2.47	2.26	1.93	1.42	0.94	0.57	0.34	0.21	0.14	0.21	0.14
	affinity pure α -O8E poly	2.73	2.70	2.63	2.48	2.27	1.90	1.41	0.93	0.57	0.34	0.21	0.14	0.21	0.14
	salt peak 739-87A	2.69	2.60	2.50	2.21	1.83	1.34	0.99	0.64	0.38	0.22	0.15	0.11	0.15	0.11
	Average	2.59	2.48	2.38	2.21	1.82	1.33	1.00	0.62	0.37	0.22	0.14	0.11	0.14	0.11
	affinity pure α -O8E poly	2.64	2.54	2.44	2.21	1.83	1.34	1.00	0.63	0.37	0.22	0.15	0.11	0.15	0.11
	acid peak 739-67B	2.46	2.39	2.40	2.34	2.08	1.73	1.29	0.81	0.49	0.29	0.19	0.13	0.19	0.13
	Average	2.65	2.66	2.61	2.45	2.14	1.76	1.30	0.82	0.48	0.29	0.19	0.13	0.19	0.13
	Average	2.56	2.53	2.51	2.39	2.11	1.74	1.30	0.81	0.49	0.29	0.19	0.13	0.19	0.13

Fig. 24

Anti-O8E mAb Binding to O8E Amino Acids
61-80 Induces Ligand Internalization

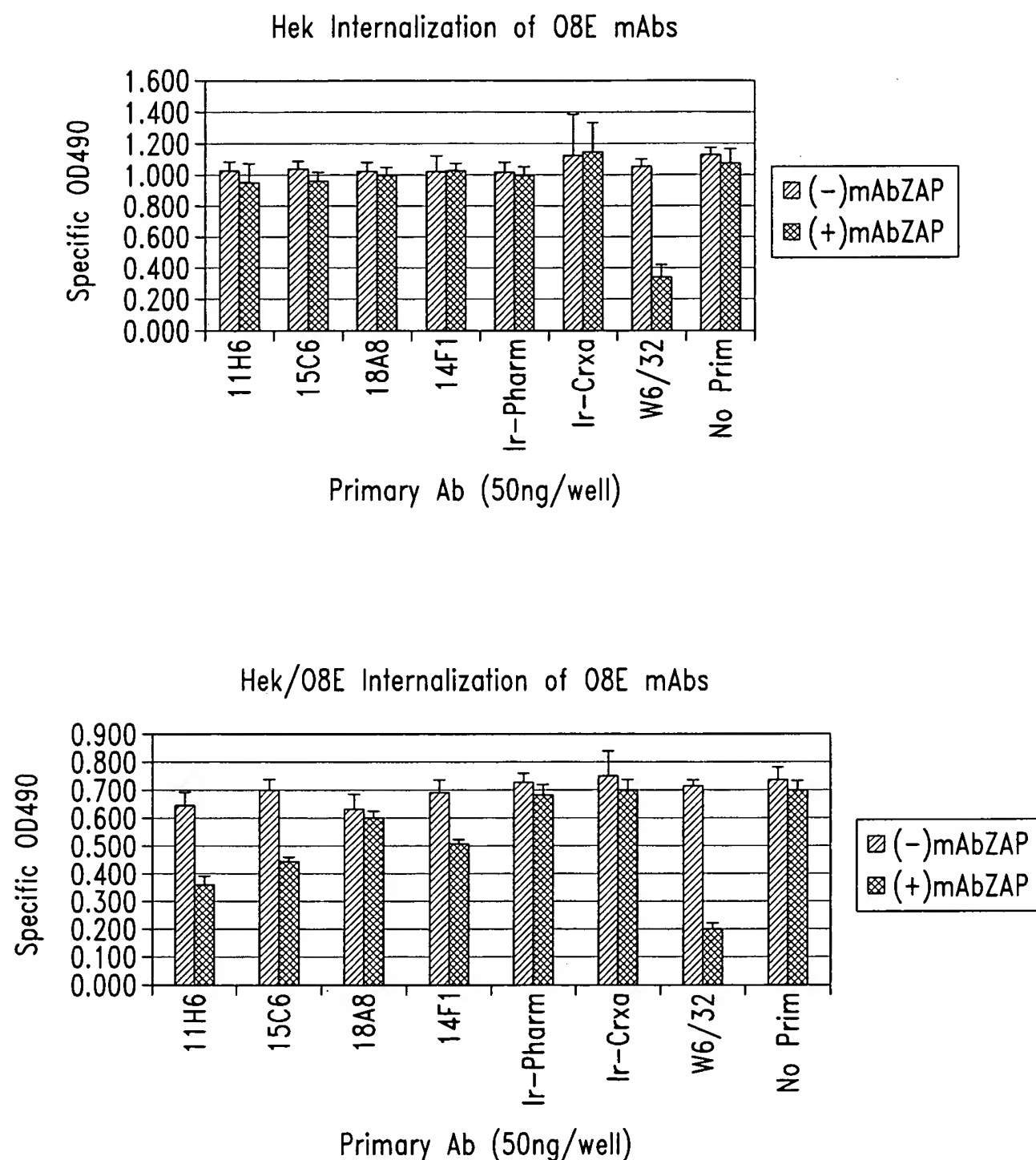


Fig. 25